

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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> 0 <  
O| 0 Intelligence  
> 0 <

FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file seq2-seq4.res made by jdelaval on Tue 15 Mar 105 10:47:43-PRST.

Query sequence being compared: US-10-693-367-14 (1-89)  
Number of sequences searched: 1  
Number of scores above cutoff: 1

Results of the initial comparison of US-10-693-367-14 (1-89) with:  
File : seq2.pep

100-  
-  
N -  
U 50-  
M -  
B -  
E -  
R -  
O -  
F 10-  
S -  
E 5-  
Q -  
U -  
N -  
C -  
E -  
S 0-  
SCORE 0 9 19 28 37 47 56 65 75 84  
STDDEV

PARAMETERS

Similarity matrix Unitary 1 K-tuple 2  
Mismatch penalty 1.00 Joining penalty 20  
Gap penalty 0.05 Window size 32  
Cutoff score 0  
Randomization group 0

SEARCH STATISTICS

Scores: Mean 84 Median 0 Standard Deviation 0.00  
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 591  
Number of sequences searched: 1  
Number of scores above cutoff: 1

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt. Sig. Frame
1. US-10-693-367-2	Sequence 2, Application US	591	84	85 0.00 0

1. US-10-693-367-14 (1-89)  
US-10-693-367-2 Sequence 2, Application US/10693367

Sequence 2, Application US/10693367  
GENERAL INFORMATION:

APPLICANT: The Trustees of Columbia University  
TITLE OF INVENTION: PARK, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE  
FILE REFERENCE: 575/55311-A-PCT-US  
CURRENT FILING DATE: 2003-10-24  
PRIORITY APPLICATION NUMBER: US/10/693,367  
PRIORITY FILING DATE: 2000-11-21  
PRIORITY APPLICATION NUMBER: PCT/US99/11341  
PRIORITY FILING DATE: 1999-05-21  
PRIORITY APPLICATION NUMBER: 09/082,737  
PRIORITY FILING DATE: 1998-05-21  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 591  
TYPE: PRT  
ORGANISM: human

Initial Score = 84 Optimized Score = 85 Significance = 0.00  
Residue Identity = 95% Matches = 85 Mismatches = 4  
Gaps = 0 Conservative Substitutions = 0

MEGKRRKRYEISAPSNFHRVHTGPDHOKFTGLPRWQSLIESARRKPLVDPACITSIQAPAKTIVR  
10 20 30 40 50 60 70  
GSKGAKDGLTLTLDBEFNMVSTRNSLRDSDPPPARARQENGMPEEPATARRGPGAGSRGPRAGHSEA  
80 90 100 110 120 130 140  
GGSGDRRRRAGPEKPKSSREGSGGPOESSRDKRPLSGPDVGTPOPGIAGAKLAAGRPFNTYPRADTDHP  
150 160 170 180 190 200 210  
SRGAGCEPHDVA PNGPSAGGLAIPSSSSSSRPPTRRGAPSPGVLGPHASRPOLA PRACTPRAVPGP  
220 230 240 250 260 270 280  
PPSPQREPORVSHQPRALQGVDPGDPRSYLDNFYIKIGESSTGIVCIATVRSAGKLVAVKMDLRKQOR  
290 300 310 320 330 340 350 360  
ELLFNEVVMRDYRHENVMYNSYVSGDELWVMVEFLGGLTDTVTTRNNEQIAAVCLAVTQALAVLH  
370 380 390 400 410 420 430  
ELLFNEVVMRDYRHENVMYNSYVSGDELWVMVEFLGGLTDTVTTRNNEQIAAVCLAVTQALAVLH  
440 450 460 470 480 490 500  
VLENDGEPFNEPPLXAMKMIKIRNLPRLNLKHKVSPSLKGLDRLVDPAPQATPAABELLKHFFLAKAG  
510 520 530 540 550 560 570  
PPASIVPLMKQNRTR  
580 590

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2005, 11:16:56 ; Search time 6.675 Seconds  
(without alignment)  
1282.890 Million cell updates/sec

Title: US-10-693-367-14

Perfect score: 452

Sequence: 1 KQRRRLLEFNEVIMRDYH.....LQALAVLHAQGVTHSDIKTD 89

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	303	67.0	540	2 T19956	hypothetical prote
2	303	67.0	542	2 T19952	hypothetical prote
3	277	61.3	544	2 S40482	serine/threonine-s
4	277	61.3	545	2 G01773	p21-activated prot
5	276	61.1	544	2 A57597	beta-p21-activated
6	269	59.5	544	2 T49376	p21 activated kina
7	266	58.8	622	2 T15467	hypothetical prote
8	265.5	58.7	525	2 S58682	protein kinase, p2
9	256	56.6	1230	2 T18256	probable serine/th
10	256	56.6	1230	2 T18259	serine/threonine p
11	255	56.4	939	2 S28394	probable serine/th
12	235.5	52.1	378	2 T26684	hypothetical prote
13	231.5	51.2	842	2 S60402	protein kinase CLA
14	227	51.1	658	2 T39500	serine/threonine-s
15	227	50.2	658	2 S60170	protein kinase Pak
16	220.5	48.8	589	2 T38086	serine/threonine-p
17	203.5	45.0	655	2 S51884	probable protein k
18	177.5	39.3	819	2 A53714	protein kinase (EC
19	167.5	37.1	829	2 T29372	hypothetical prote
20	154	34.1	1102	2 JC6316	probable protein k
21	153	33.8	836	2 B96716	MAP kinase kinase
22	151.5	33.5	1401	2 T39225	MAP kinase kinase
23	149.5	33.1	545	2 T33748	hypothetical prote
24	148.5	32.9	652	2 T39722	serine/threonine p
25	146.5	32.4	1192	2 T18611	probable serine/th
26	146	32.4	1246	2 G89287	protein H39E23.1
27	145.5	32.2	1233	2 T30989	serine/threonine p
28	145.5	32.2	1075	2 T27623	hypothetical prote
29	145.5	32.2	1080	2 T27622	hypothetical prote

30	145.5	32.2	1314	2 S19488	probable membrane
31	145	32.1	471	2 T39232	probable serine th
32	144.5	32.0	348	2 T37321	Ca2+/calmodulin-de
33	143	31.6	653	2 T34356	hypothetical prote
34	142.5	31.5	690	2 C96572	protein F12M16.4
35	141.5	31.3	1051	1 JN0051	serine/threonine-s
36	141.5	31.3	1579	2 S59801	protein kinase SSK
37	138.5	30.6	312	2 T38525	serine/threonine p
38	137.5	30.4	1062	2 S45367	protein kinase CDC
39	136	30.1	415	2 UQ2251	calcium/calmodulin
40	135.5	30.0	460	2 S58882	protein kinase Cdb
41	135.5	30.0	883	2 A96662	hypothetical prote
42	135	29.9	1206	2 T34021	protein kinase SK2
43	135	29.9	1231	2 T18532	serine/threonine pr
44	135	29.9	1233	2 T14157	serine/threonine p
45	133	29.4	1097	2 F96538	hypothetical prote

## ALIGNMENTS

RESULT 1  
T19956  
hypothetical protein C45B11.1b - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 16-Aug-2004  
C:Accession: T19956  
R:McMurray, A.  
Submitted to the EMBL Data Library, June 1996  
A:Reference number: Z19202  
A:Accession: T19956  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-540 <MTL>  
A:Cross-references: UNIPROT:Q9U3M1; EMBL:Z74029; PIDN:CAA98433.1; GSPDB:GN00023; CESP:C45B11  
C:Experimental source: clone C45B11  
C:Genetic:  
A:Gene: CESP:C45B11.1b  
A:Map position: 5  
A:Introns: 13/2; 104/2; 231/3; 367/2; 468/3  
C:Superfamily: protein kinase homology

Query Match  
Best Local Similarity 67.0%; Score 303; DB 2; Length 540;  
Matches 60; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 KQRRRLLEFNEVIMRDYHENVVEMVNSYLVGDELVMVMEFLGGALTDIVTHRMNE 60  
DB 284 KQRRRLLEFNEVIMRDYHENVVEMVNSYLVGDELVMVMEFLGGALTDIVTHRMNEP 343  
QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89  
DB 344 QIATTSQVTLGALDPLHAKVTHRIDKSP 372

RESULT 2  
T19952  
hypothetical protein C45B11.1a - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 16-Aug-2004  
C:Accession: T19952  
R:McMurray, A.  
Submitted to the EMBL Data Library, June 1996  
A:Reference number: Z19202  
A:Accession: T19952  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-542 <MTL>  
A:Cross-references: UNIPROT:Q18617; EMBL:Z74029; PIDN:CAA984429.1; GSPDB:GN00023; CESP:C45B11  
C:Experimental source: clone C45B11  
C:Genetic:  
A:Gene: CESP:C45B11.1a  
A:Map position: 5



RESULT 7  
T15467  
Hypothetical protein C09B8.7 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 16-Aug-2004  
C:Accession: T15467  
R:Stallier, L.  
Submitted to the EMBL Data Library, June 1995  
A:Description: The sequence of *C. elegans* cosmid C09B8.  
A:Reference number: S61138  
A:Accession: T15467  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-622 <STE>  
A:Cross-references: UNIPROT:Q17850; EMBL:U29612; NID:g868273; PID:g868279; PIDN:AAA68805  
A:Experimental source: strain Bristol N2  
C:Genetics:  
A:Gene: CESP.C09B8.7  
A:Introns: 107/1; 142/3; 192/1; 260/3; 291/3; 481/1; 505/3; 546/3; 570/3  
C:Superfamily: protein kinase homology

Query Match 58.8%; Score 266; DB 2; Length 622;  
Best local similarity 56.8%; Pred. No. 1,2e-16;  
Matches 50; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 2 QQRRELLFNEVIMRDYHENVEMYNISYVGDLMVMEFLGALTDIVTHTMNEQ 61  
DB 381 QPKKELINEILVMKSNKANIYVLDYLCDELVMVMEYLAGSLTDVVTETCQMEDGI 440  
DB 441 IAAVCREVLQALFLHSHRVHHRDKSD 468

QY 62 IAAVCLAVLQALAVLHAQGVHSDIKTD 89  
DB 441 IAAVCREVLQALFLHSHRVHHRDKSD 468

RESULT 8  
S58682  
Protein kinase, p21-activated (EC 2.7.1.-) - human  
N:Alternate names: protein kinase PAK65; S6/H4 kinase  
C:Species: *Homo sapiens* (man)  
C:Date: 22-Aug-1996 #sequence\_revision 06-Sep-1996 #text\_change 16-Aug-2004  
C:Accession: S58682; S55258; S55304; S58690; A57441  
R:Sellis, M.; Krause, U.J.; Bagrodia, S.; Ambrose, D.; Bokoch, G.M.; Chernoff, J.  
Submitted to the EMBL Data Library, April 1995  
A:Description: Human p21-activated protein kinases regulate actin organization in mammal  
A:Reference number: S58682  
A:Accession: S58682  
A:Molecule type: DNA  
A:Residues: 1-525 <SEL>  
A:Cross-references: UNIPROT:Q13177; EMBL:U24153; NID:g780807; PIDN:AAA65442.1; PID:g7808  
R:Martin, G.A.; Bollag, G.; McCormick, F.; Abo, A.  
EMBO J. 14, 1970-1978, 1995  
A:Title: A novel serine kinase activated by rac1/CDC42Hs-dependent autophosphorylation  
A:Reference number: S55258; MUID:95262637; PMID:7744004  
A:Accession: S55258  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 'MEFQQGNSDEL', 31-89, 'T', 91-149, 'F', 151-224, 'T', 226-328, 'R', 330-338, 340-525  
A:Accession: S55304  
A:Molecule type: protein  
A:Residues: 402-418 <MA>  
R:Martin, G.A.; Bollag, G.; McCormick, F.; Abo, A.  
EMBO J. 14, 4385, 1995  
A:Reference number: S58690; MUID:96016211; PMID:7556080  
A:Contents: erratum  
A:Accession: S58690  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-30 <MA>  
R:Benner, G.E.; Dennis, P.B.; Maesacchia, R.A.  
J. Biol. Chem. 270, 21121-21128, 1995  
A:Title: Activation of an S6/H4 kinase (PAK 65) from human placenta by intramolecular an

A:Reference number: A57441; MUID:95403344; PMID:7673144  
A:Accession: A57441  
A:Molecule type: protein  
A:Residues: 197-216/402, 'S', 404-409 <BEN>  
A:Experimental source: placenta  
C:Superfamily: protein kinase homology  
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonin  
F:247-501/Domain: protein kinase homology <KIN>  
F:255-263/Region: protein kinase ATP-binding motif  
F:197,402/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 58.7%; Score 265.5; DB 2; Length 525;  
Best local similarity 57.8%; Pred. No. 1,2e-16;  
Matches 52; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

QY 1 KQQRRELLFNEVIMRDYHENVEMYNISYVGDLMVMEFLGALTDIVTHTMNEQ 59  
DB 284 QPKKELINEILVMKSNKANIYVLDYLCDELVMVMEYLAGSLTDVVTETACMDE 343  
DB 60 EOIAAVCLAVLQALAVLHAQGVHSDIKTD 89  
DB 344 AQIAVCREVLQALFLHSHRVHHRDKSD 373

QY 61 QIAVCLAVLQALAVLHAQGVHSDIKTD 89  
DB 1049 QIGVCREVLQALFLHSHRVHHRDKSD 1077

RESULT 9  
T18256  
Probable serine/threonine-specific protein kinase (EC 2.7.1.-) - yeast (*Candida albicans*)  
C:Species: *Candida albicans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T18256  
R:Reberer, E.; Harscus, D.; Broadbent, I.D.; Clark, K.L.; Dignard, D.; Ziegelbauer, K.; S  
Proc. Natl. Acad. Sci. U.S.A. 93, 13217-13222, 1996  
A:Title: Signal transduction through homologs of the Ste20p and Ste7p protein kinases ca  
A:Reference number: Z18843; MUID:97075145; PMID:8917571  
A:Accession: T18256  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1230 <LEB>  
A:Cross-references: UNIPROT:Q13431; EMBL:L47210; NID:g2276410; PID:g2286042; PIDN:AA654  
C:Keywords: phosphotransferase; serine/threonine-specific protein kinase

Query Match 56.6%; Score 256; DB 2; Length 1230;  
Best local similarity 50.6%; Pred. No. 2e-15;  
Matches 45; Conservative 21; Mismatches 23; Indels 0; Gaps 0;

QY 1 KQQRRELLFNEVIMRDYHENVEMYNISYVGDLMVMEFLGALTDIVTHTMNEQ 60  
DB 989 QPKKELINEILVMKSNKANIYVLDYLCDELVMVMEYLAGSLTDVVTETACMDE 1048  
QY 61 QIAVCLAVLQALAVLHAQGVHSDIKTD 89  
DB 1049 QIGVCREVLQALFLHSHRVHHRDKSD 1077

RESULT 10  
T18259  
Serine/threonine protein kinase homolog - yeast (*Candida albicans*)  
C:Species: *Candida albicans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T18259  
R:Kohler, J.R.; Pink, G.R.  
Proc. Natl. Acad. Sci. U.S.A. 93, 13223-13228, 1996  
A:Title: *Candida albicans* strains heterozygous and homozygous for mutations in mitogen-  
A:Reference number: Z11116; MUID:97075146; PMID:8917572  
A:Accession: T18259  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1230 <KOH>  
A:Cross-references: UNIPROT:Q92212; EMBL:U73457; NID:g1657953; PID:g1737181; PIDN:AA638  
C:Genetics:  
A:Note: CST20

Query Match 56.6%; Score 256; DB 2; Length 1230;

Best Local Similarity 50.6%; Pred. No. 2e-15;  
Matches 45; Conservative 21; Mismatches 23; Indels 0; Gaps 0;

Qy 1 KOORRELLFNEVIMRDYRHENNVEMNSYLVDGLVWVMEFLGGALTDIYTHRMNE 60

Db 989 QOPKKEMLTIRIKWKQYRHPNLTWYIESYLVADDLWVMDYBGNLTDDVVKTEIDEG 203

Qy 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89

Db 1049 QIGVCRETLKGLKFLKSKVYIHRDIKSD 1077

## RESULT 11

S28394

Probable serine/threonine-specific protein kinase (EC 2.7.1.-) STE20 - yeast (Saccharomy

C/Species: Saccharomyces cerevisiae

C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-2004

C/Accession: S28394; S46821; A47324; A57493

R/Leberer, E.; Dignard, D.; Hancus, D.; Thomas, D.Y.; Whiteway, M.

EMBO J. 11, 4815-4824, 1992

A/Title: The protein kinase homolog Ste20p is required to link the yeast pheromone res

A/Reference number: S28394; MUID:9309855; PMID:1464311

A/Accession: S28394

A/Molecule type: DNA

A/Residues: 1-939 <LEB>

A/Cross-references: UNIPROT:Q03497; EMBL:M94719; NID:g172746; PIDN:AAA511.1; PID:g1727

R/Avellio, T.

A/Description: The sequence of S. cerevisiae cosmid L5018.

A/Reference number: S46798

A/Accession: S46821

A/Molecule type: DNA

A/Residues: 1-939 <FAV>

A/Cross-references: EMBL:U11581; NID:9508676; PIDN:AAB69747.1; PID:g508679; MIPS:YHL007C

R/Ramer, S.W.; Davis, R.W.

Proc. Natl. Acad. Sci. U.S.A. 90, 452-456, 1993

A/Title: A dominant truncation allele identifies a gene, STE20, that encodes a putative

A/Reference number: A47324; MUID:9313807; PMID:8421676

A/Accession: A47324

A/Molecule type: DNA

A/Residues: 1-18, 'S', '20-133, 'W', '135-270, 'S', '272-939 <RAM>

A/Cross-references: EMBL:U04655; NID:g172585; PIDN:AAA3038.1; PID:g172586

R/Wu, C.; Whiteway, M.; Thomas, D.Y.; Leberer, E.

J. Biol. Chem. 270, 15984-15992, 1995

A/Title: Molecular characterization of Ste20p, a potential mitogen-activated protein or

A/Reference number: A57493; MUID:95332294; PMID:7608157

A/Accession: A57493

A/Status: preliminary

A/Molecule type: protein

A/Residues: 757-784 <WTA>

C/Genetics:

Db 715 QIGAVCRETLKGLKFLKSKVYIHRDIKSD 743

## RESULT 12

T26684

hypothetical protein Y38F1A.10 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T26684

R/Wallis, J.

A/Title: submitted to the EMBL Data Library, October 1998

A/Reference number: Z20253

A/Accession: T26684

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-378 <WIL>

A/Cross-references: UNIPROT:Q9XWL8; EMBL:AL032639; PIDN:CAA21637.1; GSPDB:GN00020; CES.

C/Genetics:

A/Gene: CESP.Y38F1A.10

A/Map position: 2

C/Superfamily: kinase-related transforming protein; protein kinase homology

Query Match

Best Local Similarity 52.1%; Score 235.5; DB 2; Length 378;

Matches 45; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

Qy 2 KOORRELLFNEVIMRDYRHENNVEMNSYLVDGLVWVMEFLGGALTDIYTHRMNE 60

Db 144 QPKKEMLTIRIKWKQYRHPNLTWYIESYLVADDLWVMDYBGNLTDDVVKTEIDEG 203

Qy 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89

Db 204 QIAAVLQECUKALHFLHRSIVHRDIKSD 232

## RESULT 13

S60402

Protein kinase CLA4 (EC 2.7.1.-) - Yeast (Saccharomyces cerevisiae)

C/Species: Saccharomyces cerevisiae

C/Date: 27-Apr-1996 #sequence\_revision 17-May-1996 #text\_change 16-Aug-2004

C/Accession: S60402; S63274; S53103

R/Murphy, K.C.T.; Urbanus, U.H.M.; Planta, R.J.

Yeast 11, 1303-1310, 1995

A/Title: Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV carrying a r

A/Reference number: S60394; MUID:96132033; PMID:8553702

A/Accession: S60402

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-842 <MAU>

A/Cross-references: UNIPROT:P48562; EMBL:U23084; NID:g1050853; PIDN:AA49100.1; PID:g105

R/Maurer, C.T.C.; Urbanus, U.H.M.; Planta, R.J.

submitted to the EMBL Data Library, November 1994

Db 715 QIGAVCRETLKGLKFLKSKVYIHRDIKSD 743

## RESULT 12

T26684

hypothetical protein Y38F1A.10 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T26684

R/Wallis, J.

A/Title: submitted to the EMBL Data Library, October 1998

A/Reference number: Z20253

A/Accession: T26684

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-378 <WIL>

A/Cross-references: UNIPROT:Q9XWL8; EMBL:AL032639; PIDN:CAA21637.1; GSPDB:GN00020; CES.

C/Genetics:

A/Gene: CESP.Y38F1A.10

A/Map position: 2

C/Superfamily: kinase-related transforming protein; protein kinase homology

Query Match

Best Local Similarity 52.1%; Score 235.5; DB 2; Length 378;

Matches 45; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

Qy 2 KOORRELLFNEVIMRDYRHENNVEMNSYLVDGLVWVMEFLGGALTDIYTHRMNE 60

Db 144 QPKKEMLTIRIKWKQYRHPNLTWYIESYLVADDLWVMDYBGNLTDDVVKTEIDEG 203

Qy 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89

Db 204 QIAAVLQECUKALHFLHRSIVHRDIKSD 232

## RESULT 13

S60402

Protein kinase CLA4 (EC 2.7.1.-) - Yeast (Saccharomyces cerevisiae)

C/Species: Saccharomyces cerevisiae

C/Date: 27-Apr-1996 #sequence\_revision 17-May-1996 #text\_change 16-Aug-2004

C/Accession: S60402; S63274; S53103

R/Murphy, K.C.T.; Urbanus, U.H.M.; Planta, R.J.

Yeast 11, 1303-1310, 1995

A/Title: Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV carrying a r

A/Reference number: S60394; MUID:96132033; PMID:8553702

A/Accession: S60402

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-842 <MAU>

A/Cross-references: UNIPROT:P48562; EMBL:U23084; NID:g1050853; PIDN:AA49100.1; PID:g105

R/Maurer, C.T.C.; Urbanus, U.H.M.; Planta, R.J.

submitted to the EMBL Data Library, November 1994



A:Cross-references: SGD:S0005242; MIPS:YNL298w

A:Map position: 14L

C:Superfamily: pleckstrin repeat homology; protein kinase homology

C:Keywords: ATP; phosphotransferase

F:544-825/Domain: protein kinase homology <KIN>

Query Match 51.2%; Score 231.5; DB 2; Length 842;

Best Local Similarity 45.9%; Pred. No. 2.3e-13; Indels 9; Gaps 2;

Matches 45; Conservative 20; Mismatches 24; Indels 9; Gaps 2;

QY 1 KQORRELFNEVIMEDYHENVEMVNSYL-VGDELMVMEFLGSGALTDIV----- 52

DB 600 QOPKKEFIYNEILVMKSHHKNIYVFIIDFFYKSELVMWMEYRGSLTEVVTNNTLSG 480

QY 53 -TTRNNEBOIAVCLAVLQALAVLHAQGVHSIDIKTD 89

DB 660 NSHSPLEPOIAIVYRETCCGLKFLHDKHILHRDIKSD 697

#### RESULT 14

T39500

serine/threonine-specific protein kinase (EC 2.7.1.-) pak1-shk1 - fission yeast (Schizosaccharomyces pombe)

N:Alternate names: Ste20 homologous protein kinase 1

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 16-Aug-2004

C:Accession: T39500; T45523

R:Beck, A.; Reinhardt, R.; Lyne, M.; Rajadream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, December 1998

A:Reference number: 221859

A:Accession: T39500

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-658 <BEC>

A:Cross-references: UNIPROT:P50527; EMBL:AL034433; PIDD:CAA22347.1; GSPDB:GN00066; SPDB:

A:Experimental source: strain 972h-; cosmid c1604

R:Marcus, S.

submitted to the EMBL Data Library, April 1997

A:Reference number: 222999

A:Accession: T45523

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-658 <MAR>

A:Cross-references: EMBL:L41552; PIDD:AA52609.1

C:Genetics: 8Nk1; SPBC1604.14C

A:Gene: 8Nk1; SPBC1604.14C

A:Map position: 1

C:Superfamily: protein kinase homology

C:Keywords: hydrolase; phosphotransferase; signal transduction

Query Match 51.1%; Score 231; DB 2; Length 658;

Best Local Similarity 40.4%; Pred. No. 1.9e-13; Indels 0; Gaps 0;

Matches 36; Conservative 28; Mismatches 25; Indels 0; Gaps 0;

QY 1 KQORRELFNEVIMEDYHENVEMVNSYL-VGDELMVMEFLGSGALTDIVHTHME 60

DB 421 QOPKKEFIYNEILVMKSHHKNIYVFIIDFFYKSELVMWMEYRGSLTEVVTNNTLSG 480

QY 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89

DB 481 QIAAICKETLEGLHENGIVHRDIKSD 509

#### RESULT 15

S60170

protein kinase Pak1 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 16-Aug-2004

C:Accession: S60170

R:Oceller, S.; Miller, P.U.; Johnson, D.I.; Creasy, C.L.; Seller, M.A.; Bagrodia, S.; For

EMBO J. 14, 5908-5919, 1995

A:Title: Fission yeast Pak1(+) encodes a protein kinase that interacts with Cdc42p and

A:Reference number: S60170; MUID:96112805; PMID:8846783

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-658 <OTT>

A:Cross-references: UNIPROT:P50527; EMBL:U22371; NID:G1122910; PIDD:AA49125.1; PID:G112

C:Superfamily: protein kinase homology

C:Keywords: ATP

F:384-637/Domain: protein kinase ATP-binding motif

F:392-400/Region: protein kinase ATP-binding motif

Query Match 50.2%; Score 227; DB 2; Length 658;

Best Local Similarity 39.3%; Pred. No. 4.5e-13; Indels 0; Gaps 0;

Matches 35; Conservative 29; Mismatches 25; Indels 0; Gaps 0;

QY 1 KQORRELFNEVIMEDYHENVEMVNSYL-VGDELMVMEFLGSGALTDIVHTHME 60

DB 421 QOPKKEFIYNEILVMKSHHKNIYVFIIDFFYKSELVMWMEYRGSLTEVVTNNTLSG 480

QY 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89

DB 481 QIAAICKETLEGLHENGIVHRDIKSD 509

Search completed: March 15, 2005, 11:31:25  
Job time : 7.675 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2005, 10:58:31 ; Search time 30.1029 Seconds  
(without alignment)

1513.973 Million cell updates/sec

Title: US-10-693-367-14

Perfect score: 452  
Sequence: 1 KQGRRELFNEVIMRDYRH.....LQALAVLHAGVISHDIKTD 89

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44.3	98.0	407	2 Q8K0U2	Q8K0U2 mus musculus
2	44.3	98.0	593	1 PAK4 MOUSE	Q8Btw9 mus musculus
3	44.3	98.0	593	2 Q80Z97	Q8Btw9 mus musculus
4	44.3	98.0	597	2 Q6ZPX0	Q6ZPX0 mus musculus
5	43.6	96.5	240	2 Q8NCH5	Q8NCH5 homo sapien
6	43.6	96.5	438	2 Q8NDE3	Q8NDE3 homo sapien
7	43.6	96.5	467	2 Q9UUS8	Q9UUS8 homo sapien
8	43.6	96.5	501	2 Q8N4E1	Q8N4E1 homo sapien
9	43.6	96.5	591	1 PAK4_HUMAN	Q96013 homo sapien
10	42.1	93.1	650	2 Q90W62	Q90W62 xenopus lae
11	41.8	92.5	663	2 Q6GM11	Q6GM11 brachydanio
12	41.2	91.2	711	2 Q6NVJ4	Q6NVJ4 brachydanio
13	40.9	90.5	229	2 Q9CS71	Q9CS71 mus musculus
14	40.7	90.0	719	2 Q8C015	Q8C015 mus musculus
15	40.3	89.2	719	2 Q6RWS7	Q6RWS7 mus musculus
16	40.2	88.9	719	1 PAK7_HUMAN	Q9P286 homo sapien
17	39.9	88.3	719	2 Q8TB93	Q8TB93 homo sapien
18	39.9	88.3	681	1 PAK6_HUMAN	Q8BvB0 mus musculus
19	37.9	83.8	681	1 PAK6_HUMAN	Q9nq5 homo sapien
20	36.6	81.0	558	2 Q7QCS5	Q7QCS5 anopheles g
21	36.6	81.0	639	1 PAKM_DROME	Q9vxe5 drosophila
22	30.3	67.0	540	2 Q9U3M1	Q9U3M1 caenorhabdi
23	30.3	67.0	542	2 Q18637	Q18637 caenorhabdi
24	28.3	62.6	704	2 Q24190	Q24190 drosophila
25	28.3	62.6	704	2 Q9V113	Q9V113 drosophila
26	28.0	61.9	704	2 Q7QD76	Q7QD76 anopheles g
27	27.9	61.9	704	2 Q24213	Q24213 anopheles g
28	27.8	61.5	522	2 Q6PAZ2	Q6PAZ2 xenopus lae
29	27.7	61.3	447	2 Q86W79	Q86W79 homo sapien
30	27.7	61.3	544	1 PAK1_RAT	Q35465 rattus norv
31	27.7	61.3	545	1 PAK1_HUMAN	Q13153 homo sapien

32	27.7	61.3	545	1 PAK1 MOUSE	Q8B643 mus musculus
33	27.7	61.3	553	2 Q75561	Q75561 homo sapien
34	27.7	61.3	577	2 Q6P017	Q6P017 brachydanio
35	27.7	61.3	577	2 Q803Z0	Q803Z0 brachydanio
36	27.6	61.1	544	1 PAK3_RAT	Q62829 rattus norv
37	27.6	61.1	544	2 Q8X1R6	Q8X1R6 mus musculus
38	27.6	61.1	559	1 PAK3_HUMAN	Q75914 homo sapien
39	27.6	61.1	559	1 PAK3_MOUSE	Q61036 mus musculus
40	27.6	61.1	559	1 PAK3_PANTR	Q7Y914 pan troglod
41	27.6	61.1	559	1 PAK3_PONPY	Q7Y913 pongo pygma
42	27.6	61.1	564	2 Q8AXB4	Q8AXB4 xenopus lae
43	27.4	60.6	524	1 PAK2_HUMAN	Q13177 homo sapien
44	27.4	60.6	524	1 PAK2_MOUSE	Q8C1N4 mus musculus
45	27.4	60.6	524	1 PAK2_RABIT	Q29502 oryctolagus

#### ALIGNMENTS

RESULT 1  
ID Q8K0U2 PRELIMINARY; PRT; 407 AA.  
AC Q8K0U2;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE PAK4 protein (Fragment).  
GN Name=PAK4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange S.J.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
Krzyszewski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,  
Jones S.J., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RX Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.  
RA Strausberg R.,  
EMBL: BC030389; AAH30389.1; --  
DR HSSP; Q13153; 1F3W.  
DR MGD; MGI:1917834; Pak4.  
DR GO; GO:0005524; F-ATP binding; IEA.  
DR GO; GO:0004674; F-protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004668; P-protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Kinase like.  
DR InterPro; IPR002290; Ser\_thr\_kinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKc; 1.

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DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW ATP-binding. 1
FT NON TER
SQ SEQUENCE 407 AA; 44339 MW; 921689734DF9D710 CRC64;
Query Match
Best Local Similarity 98.0%; Score 443; DB 2; Length 407;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KOQRELLFNEVYIMRDYHENVVEMNSYVGDLMVWMEFLGALTDIVTHTRNNEE 60
DB 172 KOQRELLFNEVYIMRDYHENVVEMNSYVGDLMVWMEFLGALTDIVTHTRNNEE 231
QY 61 QIAAVCLAVLQALAVLHQAQYHSDIKTD 89
DB 232 QIAAVCLAVLQALAVLHQAQYHSDIKTD 260
RESULT 2
PAK4 MOUSE STANDARD; PRT; 593 AA.
ID PAK4 MOUSE STANDARD; PRT; 593 AA.
AC Q8BTM9;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase PAK 4 (EC 2.7.1.37) (p21-activated
DE Kinase 4) (PAK-4).
GN Name=PAK4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi H., Bono H., Kondo S.,
RA Nagai K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takehara Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watende Y., Wells C.,
RA Wilmink L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carrincci P., Hayatsu N.,
RA Hironaka-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Atakawa T., Fukuda N.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yaeumishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo W.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carrincci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Activates the JNK pathway. Implicated in the
CC reorganization of the actin cytoskeleton and in the formation of
CC filopodia (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Interacts tightly with GTP-bound but not GDP-bound
CC CDC42/p21 and weakly with Rac1 (By similarity).
CC -!- PTM: Autophosphorylated when activated by CDC42/p21 (By
CC similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. STE20
CC subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AK088512; BA040396.1; -
DR EMBL; BC048238; AA048238.1; -
DR HSSP; Q13153; 1P3M.
DR WGD; WGI:1917834; PAK4.
DR InterPro: IPR011009; Kinase like.
DR InterPro: IPR000095; PAKbox/Rho-binding.
DR InterPro: IPR000719; Prot. kinase.
DR InterPro: IPR008271; Ser/Thr/kin. AS.
DR InterPro: IPR002290; Ser/Thr/kinase.
DR InterPro: IPR011026; WASP_C.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; FALSE NEG.
KW ATP-binding; Phosphorylation; Serine/threonine-protein kinases;
KW Transferase.
FT DOMAIN 11 24 CRIB.
FT DOMAIN 25 322 Linker.
FT DOMAIN 323 574 Protein kinase.
FT NP_BIND 329 337 ATP (By similarity).
FT BINDING 352 352 ATP (By similarity).
FT ACT_SITE 442 442 Proton acceptor (By similarity).
SQ SEQUENCE 593 AA; 64622 MW; 4A9A91DD73D4C6D5 CRC64;
Query Match
Best Local Similarity 98.0%; Score 443; DB 1; Length 593;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KOQRELLFNEVYIMRDYHENVVEMNSYVGDLMVWMEFLGALTDIVTHTRNNEE 60
DB 358 KOQRELLFNEVYIMRDYHENVVEMNSYVGDLMVWMEFLGALTDIVTHTRNNEE 417

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QY 61 Q1AAVCLAVLQALAVLHAQGVHSIDIKTD 89
DB 418 Q1AAVCLAVLQALAVLHAQGVHSIDIKSD 446

RESULT 3
080297 PRELIMINARY; PRT; 593 AA.
ID 080297
AC Q80297
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE P21-activated protein kinase 4.
GN Name: Pak4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=22526742; PubMed=12529371; DOI=10.1074/jbc.M205875200;
RA Lu Y., Pan Z.Z., Devaux Y., Ray P.;
RT "p21-activated protein kinase 4 (PAK4) interacts with the keratinocyte
RT growth factor receptor and participates in keratinocyte growth factor-
RT mediated inhibition of oxidant-induced cell death."
RL J. Biol. Chem. 278:10374-10380(2003).
DR EMBL; AY217016; AAC61496.1; -.
DR HSSP; Q13153; 1F3M.
DR MGD; MGI:1917834; Pak4.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:000468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000095; PAKbox/RhoGTPase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR011026; WAF_C.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase.
SQ SEQUENCE 593 AA; 64666 MW; D7B3BD36706B4AF4 CRC64;

Query Match 98.0%; Score 443; DB 2; Length 593;
Best Local Similarity 97.8%; Pred. No. 1.7e-36;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELFNEVIMDYHENVEMVNSYLVDDELAVMEFLGALTDIVTHFRMNE 60
DB 358 KOORRELFNEVIMDYHENVEMVNSYLVDDELAVMEFLGALTDIVTHFRMNE 417
QY 61 Q1AAVCLAVLQALAVLHAQGVHSIDIKTD 89
DB 418 Q1AAVCLAVLQALAVLHAQGVHSIDIKSD 446

RESULT 4
062PX0 PRELIMINARY; PRT; 597 AA.
ID 062PX0
AC 062PX0
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MKIAA1142 protein (Fragment).
GN Name=MKIAA1142;
OS Mus musculus (Mouse).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic tail;
RX PubMed=14621295;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT III. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries."
RL DNA Res. 10:167-180(2003).
DR EMBL; AK129298; BAC98108.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.
DR GO; GO:000468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000095; PAKbox/RhoGTPase.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR011026; WAF_C.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYKC; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding.
FT NON TER 1
SQ SEQUENCE 597 AA; 64963 MW; 50C02613F77CCADA CRC64;

Query Match 98.0%; Score 443; DB 2; Length 597;
Best Local Similarity 97.8%; Pred. No. 1.7e-36;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELFNEVIMDYHENVEMVNSYLVDDELAVMEFLGALTDIVTHFRMNE 60
DB 362 KOORRELFNEVIMDYHENVEMVNSYLVDDELAVMEFLGALTDIVTHFRMNE 421
QY 61 Q1AAVCLAVLQALAVLHAQGVHSIDIKTD 89
DB 422 Q1AAVCLAVLQALAVLHAQGVHSIDIKSD 450

RESULT 5
08NCH5 PRELIMINARY; PRT; 240 AA.
ID 08NCH5
AC 08NCH5
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ90247.
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Nishikawa T., Hayaishi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hito Y., Saito K.,
RA Yamamoto U., Nakamatsu A., Nakamura Y., Kojima S., Nagahata K.,
RA Masuno Y., Ono T., Okano K., Yoshikawa Y., Aotsuba S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Nimomiya K.;
RT Submitted (MAR-02) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074728; BAC11166.1; -.
DR HSSP; Q13153; 1F3M.
```

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DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_Kinase.
DR ProDom; PD000001; Prot_Kinase; 1.
DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
SQ SEQUENCE 240 AA; 27332 MW; E3C68628BD4913B6 CRC64;

Query Match
Best Local Similarity 96.5%; Score 436; DB 2; Length 240;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KQORRELLFNEVVMRDYRHENVMNYSYLVGDELVMVMEFLGGALTDIVHTRMNEE 60
Db 5 KQORRELLFNEVVMRDYRHENVMNYSYLVGDELVMVMEFLGGALTDIVHTRMNEE 64
61 QIAAVCLAVIQAALAVLHAQGVHSDIKTD 89
65 QIAAVCLAVIQAALSVLHAQGVHSDIKSD 93

RESULT 6
Q8NDE3 PRELIMINARY; PRT; 438 AA.
AC Q8NDE3;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE Hypothetical protein DKFZps47G182.
GN Name=DKFZps47G182;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCB1_TaxID=9606;
RX TISSUE=Brain;
RA The German cDNA Consortium;
RA Wambolt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Robo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL834236; CAD38914.2; -
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
KW ATP-binding; Hypothetical protein.
SQ SEQUENCE 438 AA; 48267 MW; 4A596EBBCCE9883 CRC64;

Query Match
Best Local Similarity 95.5%; Score 436; DB 2; Length 438;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KQORRELLFNEVVMRDYRHENVMNYSYLVGDELVMVMEFLGGALTDIVHTRMNEE 60
Db 203 KQORRELLFNEVVMRDYRHENVMNYSYLVGDELVMVMEFLGGALTDIVHTRMNEE 262
61 QIAAVCLAVIQAALAVLHAQGVHSDIKTD 89
263 QIAAVCLAVIQAALSVLHAQGVHSDIKSD 291

RESULT 7
Q9ULS8 PRELIMINARY; PRT; 467 AA.
AC Q9ULS8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE KIAA1142 protein (Fragment).
GN Name=KIAA1142;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20039618; PubMed=10574461;
RA Hiroseawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
RT "Characterization of cDNA clones selected by the Genemark analysis
RT from size-fractionated cDNA libraries from human brain.";
RL DNA Res. 6:329-336(1999).
DR EMBL; AB032968; BA86456.1; -.
DR HSSP; Q3153; 1P3W.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR011026; WASP_C.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; Prot_Kinase; 1.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS50107; PROTEIN KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding.
FT NON TER
SQ SEQUENCE 467 AA; 51464 MW; EC342B8F5C5E3940 CRC64;

Query Match
Best Local Similarity 96.5%; Score 436; DB 2; Length 467;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KQORRELLFNEVVMRDYRHENVMNYSYLVGDELVMVMEFLGGALTDIVHTRMNEE 60
Db 232 KQORRELLFNEVVMRDYRHENVMNYSYLVGDELVMVMEFLGGALTDIVHTRMNEE 291
61 QIAAVCLAVIQAALAVLHAQGVHSDIKTD 89
292 QIAAVCLAVIQAALSVLHAQGVHSDIKSD 320

RESULT 8
Q8N4E1 PRELIMINARY; PRT; 501 AA.
AC Q8N4E1;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE PAK4 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCB1_TaxID=9606;
RX TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Casavant T.L., Schaefer T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.J.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Chae S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McManus P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
```

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywiński M.I., Skalska U., Smallie D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.,  
 RT Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Straubeberg R.,  
 RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC034511; AAH34511.1; -.  
 DR HSSP; Q13153; 1F3W.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004674; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR011009; Kinase like.  
 DR InterPro; IPR000095; PAKbox/RhoGTPase.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00786; PBD; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00285; PBD; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR PROSITE; PS50108; CRIB; 1.  
 DR PROSITE; PS50107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW ATP-binding.  
 SQ SEQUENCE 501 AA; 54940 MW; 6EE6240EC65E79D CRC64;

Query Match 96.5%; Score 436; DB 2; Length 501;  
 Best Local Similarity 95.5%; Pred. No. 7,4e-36;  
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQQRRELLFNEVIMNDYRHNNVEMNSYLVDGLVWVEFLGALTDIVHTNNNEE 60  
 DB 266 KQQRRELLFNEVIMNDYRHNNVEMNSYLVDGLVWVEFLGALTDIVHTNNNEE 325  
 QY 61 QIAVCLAVYQALAVLAHAGVTHSDIKTD 89  
 DB 326 QIAVCLAVYQALVSLVLAQGVHSDIKSD 354

RESULT 9  
 PAK4\_HUMAN STANDARD; PRT; 591 AA.  
 AC 096013; Q9BUJ3;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE 05-JUL-2004 (Rel. 44, Last annotation update).  
 DE Serine/threonine-protein kinase PAK 4 (EC 2.7.1.37) (p21-activated  
 DE kinase 4) (PAK-4).  
 GN Name=PAK4;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=99043860; PubMed=982598; DOI=10.1093/emboj/17.22.6527;  
 RA Abo A., Qu J., Cammarano M.S., Dan C., Fritsch A., Baud V.,  
 RA Bellais B., Minden A.,  
 RT "PAK4, a novel effector for Cdc42Hs, is implicated in the  
 RT reorganization of the actin cytoskeleton and in the formation of  
 RT filopodia.";  
 RL EMBO J. 17:6527-6540(1998).  
 RN [2]  
 RN SEQUENCE FROM N.A. (ISOFORM 1).  
 RP Melnick M.B.,

RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE=Eye, Pancreas, and Placenta;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schlier G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Tohyuki S., Carninci P., Millar S.J.,  
 RA Raba S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Guntaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Pahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Smallie D.E.,  
 RA Butterfield Y.S.N., Krzywiński M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-1- FUNCTION: Activates the JNK pathway. Implicated in the  
 CC reorganization of the actin cytoskeleton and in the formation of  
 CC filopodia.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- SUBUNIT: Interacts tightly with GTP-bound but not GDP-bound  
 CC -1- CDC42/p21 and weakly with RAC1.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=O96013-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=O96013-2; Sequence=VSP\_004892, VSP\_004893;  
 CC Note=No experimental confirmation available;  
 CC -1- TISSUE SPECIFICITY: Highest expression in prostate, testis and  
 CC colon.  
 CC -1- PTM: Autophosphorylated when activated by CDC42/p21.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. STE20  
 CC subfamily.  
 CC -1- SIMILARITY: Contains 1 CRIB domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

EMBL; AT011855; CA09820.1; -  
 DR EMBL; AF005046; AAD01210.1; -  
 DR EMBL; BC002921; AAH02921.1; -  
 DR EMBL; BC013681; AAH13681.1; -  
 DR EMBL; BC025282; AAH25282.1; -  
 DR HSSP; Q13153; 1F3W.  
 DR GeneW; HGNC:16059; PAK4.  
 DR H-InvDB; HIT0015110; -.  
 DR MIM; 605451; -.  
 DR GO; GO:0005794; C:Golgi apparatus; TAS.  
 DR GO; GO:0006928; P:cell motility; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR011009; Kinase like.  
 DR InterPro; IPR000095; PAKbox/RhoGTPase.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR011026; WASP\_C.  
 DR Pfam; PF00786; PBD; 1.  
 DR Pfam; PF00069; Pkinase; 1.

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DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR PROSITE; PS00220; S_TKC; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50108; PROTEIN_KINASE_ST; FALSE_NEG.
KW Alternative splicing; ATP-binding; Phosphorylation;
KW Serine/threonine-protein kinase; transferase.
FT DOMAIN 11
FT DOMAIN 25
FT DOMAIN 320
FT NP_BIND 321
FT NP_BIND 327
FT BINDING 350
FT ACT_SITE 440
FT VASAPLIC 120
FT VASAPLIC 120
FT VASAPLIC 120
FT VASAPLIC 121
FT VASAPLIC 285
SQ SEQUENCE 591 AA; 64071 MW; 04C2A5C0B06427D5 CRC64;

Query Match 96.5%; Score 436; DB 1; Length 591;
Best Local Similarity 95.5%; Pred. No. 8.8e-36;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVYIMRDYRHEVNVEMNSYLVGDELWVMEFLGALTDIVHTRNNEE 60
DB 356 KOORRELLFNEVYIMRDYRHEVNVEMNSYLVGDELWVMEFLGALTDIVHTRNNEE 60
QY 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89
DB 416 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 444

RESULT 10
Q90W62 PRELIMINARY; PRT; 650 AA.
AC Q90W62;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PAF5 protein.
GN Name=PAF5.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stage VI oocyte;
RA Cau J., Faure S., Delbert C., Morin N.;
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; A0277826; CAC40979.1; -.
DR HSSP; Q3153; 1F3M.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004668; F:protein amino acid phosphorylation; IEA.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding.
SQ SEQUENCE 650 AA; 73736 MW; 9274DC6ACAD4A081 CRC64;

Query Match 93.1%; Score 421; DB 2; Length 650;
Best Local Similarity 89.9%; Pred. No. 3.2e-34;
Matches 80; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVYIMRDYRHEVNVEMNSYLVGDELWVMEFLGALTDIVHTRNNEE 60
DB 415 KOORRELLFNEVYIMRDYRHEVNVEMNSYLVGDELWVMEFLGALTDIVHTRNNEE 474
QY 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89
DB 475 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 503

RESULT 11
Q6GM11 PRELIMINARY; PRT; 663 AA.
ID Q6GM11;
AC Q6GM11;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Zgc:92014.
GN ORFNames=zgc:92014;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Caavant T.L., Prange C.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
RA Bork S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield J.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerker A., Schein J.E.,
RA Jones S.J., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC074067; AAH74067.1; -.
DR ZFIN; ZDB-GENE-040704-69; zgc:92014.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004668; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011003; Kinase_Ilike.
DR InterPro; IPR000095; PAKox/Rhodning.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_thr_kinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

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KM ATP-binding. 663 AA; 74760 MW; 61P86F8876840550 CRC64;  
SQ SEQUENCE

Query Match 92.5%; Score 418; DB 2; Length 663;  
Best Local Similarity 89.9%; Pred. No. 6,7e-34;  
Matches 80; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVYIMDHYHENVVEMVNSYLVGDDELVMVMEFLGGALTDIYHTMNEE 60  
|||||  
428 KOORRELLFNEVYIMDHYHENVVEMVNSYLVGDDELVMVMEFLGGALTDIYHTMNEE 487

DB 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89  
|||  
488 QISTVCLSVLKALSVLHSGGVHRIKSD 516

RESULT 12

Q6NVJ4 PRELIMINARY; PRT; 711 AA.  
ID 06NVJ4  
AC 06NVJ4:  
DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
DE Hypothetical protein zgc:76890.  
GN ORFNames=zgc:76890;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
NCBI\_TaxID=7955;  
[1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Tothiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimm J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalek U., Smalins D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Maiz M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Strausberg R.;  
RX Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL, BC068016; AAH68016.1; -;  
DR ZFIN, ZDB-GENE-040426-2085; zgc:76890.  
DR GO, GO:0005524; F-ATP binding; IEA.  
DR GO, GO:0004674; F-protein serine/threonine kinase activity; IEA.  
DR GO, GO:0004713; F-protein-tyrosine kinase activity; IEA.  
DR GO, GO:0006468; P-protein amino acid phosphorylation; IEA.  
DR InterPro, IPR001009; Kinase, like.  
DR InterPro, IPR000095; PAKbox/RhoGAP.  
DR InterPro, IPR000719; Prot. kinase.  
DR InterPro, IPR002290; Ser\_Thr\_kinase.  
DR InterPro, IPR001245; Tyr\_kinase.  
DR InterPro, IPR011026; WASP\_C.  
DR Pfam, PF00786; PBD; 1.  
DR Pfam, PF00069; Pkinase; 1.

DR Prodom; PD0000001; Prot. Kinase; 1.  
DR SMART; SM00285; PBD; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR SMART; SM00219; TYKc; 1.  
DR PROSITE; PS00108; CRIB; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
KM ATP-binding; Hypothetical protein.  
SQ SEQUENCE 711 AA; 78613 MW; D09E7B8D579D211B CRC64;  
Query Match 91.2%; Score 412; DB 2; Length 711;  
Best Local Similarity 88.8%; Pred. No. 2.9e-33;  
Matches 79; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVYIMDHYHENVVEMVNSYLVGDDELVMVMEFLGGALTDIYHTMNEE 60  
|||||  
476 KOORRELLFNEVYIMDHYHENVVEMVNSYLVGDDELVMVMEFLGGALTDIYHTMNEE 535

DB 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89  
|||  
536 QIATVCLSVLKALSVLHSGGVHRIKSD 564

RESULT 13

Q9CS71 PRELIMINARY; PRT; 229 AA.  
ID Q9CS71  
AC Q9CS71:  
DT 01-JUN-2001 (T-EMBLrel. 17, Created)  
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)  
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
DE Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched  
DE library, clone:573048107 product:SERINE/THREONINE-PROTEIN KINASE PAK  
DE 4 (EC 2.7.1.-) (P21-ACTIVATED KINASE 4) (PAK-4) homolog  
DE (Fragment).  
GN Name=PAK4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
NCBI\_TaxID=10090;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RL "High-efficiency full-length cDNA cloning";  
RL Meth. Enzymol. 303:19-44(1999).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN PANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
[3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RA The PANTOM Consortium;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
[4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
[5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;

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RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shiba K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:11757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi U., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arahata T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuo M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirao K., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami T., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamori T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR HSSP; Q13153; 1P3M.
DR MGD; MGI:1917834; Pak4.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR Pfam; PF00069; Prot_Kinase.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KM Kinase.
FT NON_TER
SQ
Query Match 229 AA; 25896 MW; D9CF2CA73CED941E CRC64;
Best Local Similarity 90.5%; Score 409; DB 2; Length 229;
Matches 80; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 8 LENEVYIMRDYRHENVENWYNSYLVGDELVMYMELEGALTDIYTHRNNEEOJAAVCL
DB 1 LENEVYIMDYRHENVENWYNSYLVGDELVMYMELEGALTDIYTHRNNEEOJAAVCL
QY 68 AVTQALAVYHAQGVYHSDIKTD 89
DB 61 AVTQALAVYHAQGVYHSDIKTD 82
RESULT 14
Q8C015 PRELIMINARY; PRT; 719 AA.
AC Q8C015;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length
DE enriched library, clone:6430627N20 Product:SERINE/THREONINE-PROTEIN
DE KINASE PAK 5 (EC 2.7.1.-) (P21-ACTIVATED KINASE 5) (PAK-5)
DE homolog.
GN Name=PAK7;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;

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RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shiba K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:11757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA Adachi U., Aizawa K., Akimura T., Arahata T., Bono H., Carninci P.,
RA Fukuda S., Furuo M., Hayatsu N., Hiramoto K., Hirao K., Hori F.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirao K., Hori F.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa T., Kato H.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohata N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka T., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR HSSP; Q13153; 1P3M.
DR MGD; MGI:1920334; Pak7.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006916; F:anti-apoptosis; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000095; PAKox/rho-binding.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR011026; WASP_C.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; Kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1_kinase; 1.
DR SMART; SM00220; s_Tkc; 1.

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Search completed: March 15, 2005, 11:30:27  
 Job time : 30.1029 secs

DR PROSITE; PSS0108; CRIB; 1.  
 DR PROSITE; PSS0107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PSS0011; PROTEIN\_KINASE\_DOM; 1.  
 KW ATP-binding; Kinase.  
 SQ SEQUENCE 719 AA; 80948 MW; 5E16D2318C238C8D CRC64;

Query Match 90.0%; Score 407; DB 2; Length 719;  
 Best Local Similarity 87.6%; Pred. No. 9.5e-33;  
 Matches 78; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 KOQRRELLFNEVIMRDYHENVEMVNSYLVGDELVMVEFLEGALTDIVHTRMNEE 60  
 DB 484 KOQRRELLFNEVIMRDYHENVEMVNSYLVGDELVMVEFLEGALTDIVHTRMNEE 543

QY 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89  
 DB 544 QIAVCLSVLKALSYLHNGVIRHDIKSD 572

## RESULT 15

Q6RWS7 PRELIMINARY; PRT; 719 AA.  
 AC Q6RWS7;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE P21-activated kinase 5.  
 GN Name=Pak7;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=Brain;  
 RX MEDLINE=22879895; PubMed=14517284;  
 RX DOI=10.1126/MCB.23.20.7134-7142.2003;  
 RA Li X., Minden A.;  
 RT "Targeted disruption of the gene for the PAKS kinase in mice.";  
 RL Mol. Cell. Biol. 23:7134-7142(2003).  
 DR GO; GO:0005739; Cytochrome oxidase; IDA.  
 DR GO; GO:0004674; F-protein serine/threonine kinase activity; IDA.  
 DR GO; GO:0006916; P-anti-apoptosis; IDA.  
 DR InterPro; IPR011009; Kinase\_like.  
 DR InterPro; IPR000095; PAKbox/Rhodpung.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_Thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR InterPro; IPR011026; WASP\_C.  
 DR Pfam; PF00786; PBD; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00285; PBD; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR SMART; SM00219; TYKc; 1.  
 DR PROSITE; PSS0108; CRIB; 1.  
 DR PROSITE; PSS0107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PSS0011; PROTEIN\_KINASE\_DOM; 1.  
 KW ATP-binding; Kinase.  
 SQ SEQUENCE 719 AA; 80937 MW; 3A0159B9F14D34C7 CRC64;

Query Match 89.2%; Score 403; DB 2; Length 719;  
 Best Local Similarity 86.5%; Pred. No. 2.4e-32;  
 Matches 77; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 KOQRRELLFNEVIMRDYHENVEMVNSYLVGDELVMVEFLEGALTDIVHTRMNEE 60  
 DB 484 KOQRRELLFNEVIMRDYHENVEMVNSYLVGDELVMVEFLEGALTDIVHTRMNEE 543

QY 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89  
 DB 544 QIAVCLSVLKALSYLHNGVIRHDIKSD 572

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: March 15, 2005, 10:56:56 ; Search time 30.6265 Seconds  
(without alignments)  
1123.919 Million cell updates/sec

Title: US-10-693-367-14

Perfect score: 452  
Sequence: 1 KQGRRELLFNEVIMRDYR.....LQALVLAAGVYHSIDIKTD 89

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Database :

A\_Geneseq.16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	452	100.0	89	AAV59139	AAV59139 Mouse ser
2	443	98.0	593	ADJ96654	Adj96654 Human bre
3	436	96.5	240	AAW93287	Aaw93287 Human pol
4	436	96.5	240	ADC37303	Adc37303 Nucleic f
5	436	96.5	240	ADL30760	Adl30760 Human pro
6	436	96.5	250	AAV59129	AAV59129 Human PAK
7	436	96.5	293	ADL15851	Adel15851 PAK4KD pr
8	436	96.5	398	AAV55941	Aay55941 Human PAK
9	436	96.5	438	ADC37305	Adc37305 Nucleic f
10	436	96.5	501	ADC37309	Adc37309 Nucleic f
11	436	96.5	522	ABM84642	Abm84642 Human dia
12	436	96.5	522	ABM84644	Abm84644 Human dia
13	436	96.5	522	ABM84645	Abm84645 Human dia
14	436	96.5	588	ADH23359	Adh23359 Human p21
15	436	96.5	591	AAV55964	Aay55964 Pull leng
16	436	96.5	591	AAV59128	AAV59128 Human ser
17	436	96.5	591	ADC37307	Adc37307 Nucleic f
18	436	96.5	591	ADH89973	Adh89973 Human can
19	436	96.5	591	ADP45079	Adp45079 Human kin
20	436	96.5	591	ADH23352	Adh23352 Human p21
21	436	96.5	591	ABM82101	Abm82101 Tumour-as
22	436	96.5	620	ABG19308	Abg19308 Novel hum
23	432	95.6	438	ADR39763	Adr39763 Human kin
24	416	92.0	338	ADL22704	Adl22704 Human dia
25	407	90.0	547	AA67825	Aag67825 Human p21

26	407	90.0	719	4	AAV38963	Aam38963 Human pol
27	407	90.0	719	7	ADJ83007	Adj83007 Murine ma
28	402	88.9	457	8	ADH42207	Adh42207 Novel hum
29	402	88.9	457	8	ADH42215	Adh42215 Novel hum
30	402	88.9	457	8	ADH42211	Adh42211 Novel hum
31	402	88.9	457	8	ADH42217	Adh42217 Novel hum
32	402	88.9	457	8	ADH42213	Adh42213 Novel hum
33	402	88.9	580	7	ADW04603	Adw04603 Human pro
34	402	88.9	632	4	ABM85788	Abm85788 Human kin
35	402	88.9	719	4	AAV65705	Aab65705 Novel pro
36	402	88.9	719	4	AAE02187	Aae02187 Human p21
37	402	88.9	719	7	ADC37451	Adc37451 Nucleic f
38	402	88.9	719	7	ADF45080	Adf45080 Human kin
39	402	88.9	719	7	ADJ83008	Adj83008 Human mam
40	402	88.9	719	8	ADJ29314	Adj29314 Human MAR
41	379	83.8	311	4	AAV20336	Aab20336 Human PAK
42	379	83.8	636	8	ADQ65328	Adq65328 Novel hum
43	379	83.8	641	5	AAE16269	Aae16269 Human kin
44	379	83.8	681	2	AAV55940	Aay55940 Human PAK
45	379	83.8	681	3	AAV03967	Aab03967 Signal tr

## ALIGNMENTS

## RESULT 1

AAV59139  
ID AAV59139 standard; protein, 89 AA.

AAV59139;  
XX

08-MAR-2000 (first entry)  
XX

Mouse serine/threonine kinase, PAK4 partial protein sequence.  
DE

PAK4, serine/threonine kinase, GRPase; intracellular signal cascade; Rac;  
KW Cdc42H; morphogenesis; mitogenesis; JNK; p38 MAP kinase; mouse;

actin polymerization; filopodia; cancer; arthritis.  
KW

Mus sp.  
OS

WO9963073-A1.  
XX

09-DEC-1999.  
XX

21-MAY-1999; 99WO-US011341.  
XX

21-MAY-1998; 98US-00082737.  
XX

(UYCO) UNIV COLUMBIA NEW YORK.  
PA

Minden A;  
PI

WPI; 2000-072881/06.  
DR

N-PSDB; AA240658.  
XX

Novel mammalian nucleic acid useful for treating cancer and arthritis.  
PT

Disclosure; Page 44; 95pp; English.  
PS

The invention relates to an isolated mammalian nucleic acid that encodes PAK4, a novel serine/threonine kinase or its mutant homolog. PAK4 is an effector for the GRPases Rac and Cdc42Hs which are involved in intracellular signal cascades, morphogenesis and mitogenesis, and activate the JNK and p38 MAP kinase pathways. Inhibiting interaction of PAK4 with these enzymes will thus result in inhibition of actin polymerization and formation of filopodia. The PAK4 nucleic acid used for recombinant production of the protein, and as a source of probes for identifying homologous sequences and of (anti)sense oligonucleotides for inhibiting PAK4 expression. The protein, or its fragments, are used to raise specific antibodies and these are useful as ligands for therapeutic inhibition of interaction between PAK4 and its native binding partners. Inhibition of PAK4 activity or expression is used for treatment of cancer

CC and arthritis. The present sequence represents the partial sequence of  
CC mouse PAK4  
XX  
SQ Sequence 89 AA;

Query Match  
Best Local Similarity 100.0%; Score 452; DB 3; Length 89;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQRRRELLFNEVVIIMRDYRHNEMVNSYLVGDELWVMEFLREGALTDIVTHRMNEE 60  
DB 1 KQRRRELLFNEVVIIMRDYRHNEMVNSYLVGDELWVMEFLREGALTDIVTHRMNEE 60  
QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89  
DB 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89

RESULT 2  
ADJ96654  
ID ADJ96654 standard; protein; 593 AA.  
XX  
AC ADJ96654;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human sterile protein kinase STE20 Paks\_m protein SeqID 111.

XX kinase; human; tyrosine protein kinase; serine/threonine protein kinase;  
XX PK; STK; gene therapy; cancer; immune-related disease;  
XX cardiovascular disease; brain; neuronal associated disease; metabolic;  
XX inflammatory disorder; cytosolic; neuroprotective; immunomodulator;  
XX antiinflammatory; enzyme; sterile protein kinase STE20; Paks\_m.  
XX  
OS Homo sapiens.  
XX 59.

PN WO2004006838-A2.

PD 22-JAN-2004.

PF 15-JUL-2003; 2003WO-US021730.

PR 15-JUL-2002; 2002US-0395632P.

PA (SUGEN-) SUGEN INC.

PI Whyte D, Manning G, Caenepeel S;

DR WPI, 2004-122753/12.

DR N-PSDB; ADJ96588.

XX New nucleic acid molecule encoding a kinase polypeptide, useful for  
XX preparing a composition for treating diseases or disorders, e.g., cancer,  
XX or neurological, immunological or inflammatory disorders.

Claim 1; SEQ ID NO 111; 366pp; English.

CC This invention relates to a novel isolated, enriched or purified nucleic  
CC acid molecule that encodes a kinase polypeptide. Specifically, it relates  
CC to human tyrosine and serine/threonine protein kinases (PK's and STK's),  
CC as well as protein kinase-like enzymes. The present invention describes  
CC screening methods to identify agonists, antagonists and antibodies that  
CC can be used to modulate the activity or function of the mammalian kinase  
CC enzymes. As such, these compositions can be used for gene therapy  
CC purposes to treat diseases or disorders including cancer, immune-related  
CC diseases, cardiovascular disease, brain or neuronal associated disease,  
CC metabolic and inflammatory disorders. Accordingly, they exhibit  
CC cytosolic, neuroprotective, immunomodulator and antiinflammatory  
CC activities. This polypeptide sequence is a human kinase protein sequence  
CC of the invention.

XX Sequence 593 AA;  
SQ

Query Match  
Best Local Similarity 98.0%; Score 443; DB 8; Length 593;  
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQRRRELLFNEVVIIMRDYRHNEMVNSYLVGDELWVMEFLREGALTDIVTHRMNEE 60  
DB 358 KQRRRELLFNEVVIIMRDYRHNEMVNSYLVGDELWVMEFLREGALTDIVTHRMNEE 417  
QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89  
DB 418 QIAAVCLAVLQALAVLHAQGVTHSDIKSD 446

RESULT 3  
AAM93297  
ID AAM93297 standard; protein; 240 AA.  
XX  
AC AAM93297;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human polypeptide, SEQ ID NO: 2793.

XX Human, full length cDNA; cDNA synthesis; oligo-capping.  
XX  
OS Homo sapiens.  
XX  
PN EP1130094-A2.  
XX  
PD 05-SEP-2001.  
XX  
PF 07-JUL-2000; 2000EP-00114089.

XX 08-JUL-1999; 99JP-00194486.  
XX 11-JAN-2000; 2000JP-00118774.  
XX 02-MAY-2000; 2000JP-00183765.  
XX  
PA (HELI-) HELIX RES INST.

XX Ota T, Nishikawa T, Isegai T, Hayashi K, Ishii S, Kawai Y;  
XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX WPI; 2001-524255/58.  
XX N-PSDB; AAK94217.

XX PT 830 Primers useful for synthesizing full length cDNA clones and their use  
XX in genetic manipulation.  
XX  
PS Claim 8; SEQ ID NO 2793; 1380pp + Sequence Listing; English.

CC The invention relates to primers for synthesizing full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been isolated  
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
CC been determined. Primers for synthesizing the full length cDNA are useful  
CC for clarifying the function of the protein encoded by the cDNA. The full  
CC length clones were obtained by construction of full length enriched cDNA  
CC libraries that were synthesised by the oligo-capping method. The primers  
CC enable the production of the full length cDNA easily without any special  
CC methods. The present sequence is a polypeptide encoded by a full length  
CC human cDNA of the invention. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in CD-ROM  
XX format directly from EPO

SQ Sequence 240 AA;

Query Match  
Best Local Similarity 96.5%; Score 436; DB 4; Length 240;  
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQRRRELLFNEVVIIMRDYRHNEMVNSYLVGDELWVMEFLREGALTDIVTHRMNEE 60  
DB 5 KQRRRELLFNEVVIIMRDYRHNEMVNSYLVGDELWVMEFLREGALTDIVTHRMNEE 64

QY 61 QIAAACLAVLQALAVLHAQGVTHSDIKTD 89  
 DB 65 QIAAACLAVLQALSVLHAQGVTHSDIKSD 93

RESULT 4  
 ADC37303  
 ID ADC37303 standard; protein; 240 AA.

AC ADC37303;

DT 18-DEC-2003 (first entry)

DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 136.

KM Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;  
 cancer; infectious disease; bone disease; AIDS;

KM neurodegenerative disease; ischemic disorder; Anti-inflammatory;  
 Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;  
 Neuroprotective; Nootropic; Cardiant; Gene therapy; human.

OS Homo sapiens.

PN WO2003048202-A2.

PD 12-JUN-2003.

PF 03-DEC-2002; 2002WO-JP012644.

PR 03-DEC-2001; 2001JP-00368692.

PR 03-DEC-2001; 2001US-0335829P.

PR 03-OCT-2002; 2002JP-00291302.

PR 04-OCT-2002; 2002US-0415769P.

PA (ASAH) ASAHI KASEI KK.

PI Matcoda A, Muramatsu S;

DR WPI; 2003-505282/47.

DR N-PSDB; ADC37302.

PT New purified protein that activates nuclear factor kappa B (NF-kappaB),  
 useful for treating inflammation, autoimmune diseases, cancers,  
 infectious diseases, bone diseases, AIDS, neurodegenerative diseases or  
 ischemic disorders.

PS Claim 1; SEQ ID NO 136; 938pp; English.

CC The present invention relates to novel proteins and their coding  
 CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-  
 CC kappaB). The proteins and their coding sequences are useful for treating  
 CC a disease associated with NF-kappaB activation, such as inflammation,  
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,  
 CC neurodegenerative diseases, or ischemic disorders.

XX Sequence 240 AA;

Query Match 96.5%; Score 436; DB 7; Length 240;  
 Best Local Similarity 95.5%; Pred. No. 5, 2e-48;  
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVVIMRDYRHENVEMVNSYLVGDELVMVMEFLGGALTDIVTHTMNEE 60  
 DB 5 KOORRELLFNEVVIMRDYRHENVEMVNSYLVGDELVMVMEFLGGALTDIVTHTMNEE 64

QY 61 QIAAACLAVLQALAVLHAQGVTHSDIKTD 89  
 DB 65 QIAAACLAVLQALSVLHAQGVTHSDIKSD 93

RESULT 5  
 ADL30760

ID ADL30760 standard; protein; 240 AA.  
 AC ADL30760;

DT 20-MAY-2004 (first entry)

DE Human protein encoded by a full length cDNA clone segid 2793.

KM human; medicine; signal transduction; glycoprotein; transcription;  
 KW oligo-capping method.

OS Homo sapiens.

PN EPI396543-A2.

PD 10-MAR-2004.

PF 07-JUL-2000; 2003BP-00025638.

PR 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-00118774.

PR 02-MAY-2000; 2000JP-00183865.

PR 07-JUL-2000; 2000BP-00114089.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

DR WPI; 2004-204755/20.

DR N-PSDB; ADL30759.

PT New oligonucleotide primers (830 CDNA) useful for synthesizing full  
 PT length human CDNA.

PS Example 1; SEQ ID NO 2793; 1340pp; English.

CC This invention relates to a novel primers useful for synthesizing full  
 CC length CDNA molecules that encode human proteins. Specifically, it refers  
 CC to secretory or membrane proteins that are potential therapeutic agents/  
 CC target molecules in the field of medicine, and in particular genes  
 CC encoding proteins that are associated with signal transduction,  
 CC glycoproteins and transcription. The present invention describes a method  
 CC for efficiently cloning a full length human CDNA from both the 5' and 3'  
 CC ends using the oligo-capping method. This polypeptide sequence is a full  
 CC length human protein of the invention.

XX Sequence 240 AA;

Query Match 96.5%; Score 436; DB 8; Length 240;  
 Best Local Similarity 95.5%; Pred. No. 5, 2e-48;  
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVVIMRDYRHENVEMVNSYLVGDELVMVMEFLGGALTDIVTHTMNEE 60  
 DB 5 KOORRELLFNEVVIMRDYRHENVEMVNSYLVGDELVMVMEFLGGALTDIVTHTMNEE 64

QY 61 QIAAACLAVLQALAVLHAQGVTHSDIKTD 89  
 DB 65 QIAAACLAVLQALSVLHAQGVTHSDIKSD 93

RESULT 6  
 AA59129  
 ID AA59129 standard; protein; 250 AA.

AC AA59129;

DT 08-MAR-2000 (first entry)

DE Human PAK4 kinase domain fragment.

KM PAK4; serine/threonine kinase; GTPase; intracellular signal cascade; Rac;

KW Cdc42H; morphogenesis; mitogenesis; JNK; p38 MAP kinase; human;  
 KM actin polymerization; filopodia; cancer; arthritis; kinase domain.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9963073-A1.  
 XX  
 PD 09-DEC-1999.  
 XX  
 PF 21-MAY-1999; 99WO-US011341.  
 XX  
 PR 21-MAY-1998; 98US-00082737.  
 XX  
 PA (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX  
 PI Minden A;  
 XX  
 DR WPI; 2000-072881/06.  
 XX  
 PT Novel mammalian nucleic acid useful for treating cancer and arthritis.  
 XX  
 PS Disclosure; Fig 1c; 95pp; English.  
 XX  
 CC The invention relates to an isolated mammalian nucleic acid that encodes  
 CC PAK4, a novel serine/threonine kinase or its mutant homolog. PAK4 is an  
 CC effector for the GTPases Rac and Cdc42Hs which are involved in  
 CC intracellular signal cascades, morphogenesis and mitogenesis, and  
 CC activate the JNK and p38 MAP kinase pathways. Inhibiting interaction of  
 CC PAK4 with these enzymes will thus result in inhibition of actin  
 CC polymerization and formation of filopodia. The PAK4 nucleic acid used for  
 CC recombinant production of the protein, and as a source of probes for  
 CC identifying homologous sequences and of (anti)sense oligonucleotides for  
 CC inhibiting PAK4 expression. The protein, or its fragments, are used to  
 CC raise specific antibodies and these are useful as ligands for therapeutic  
 CC inhibition of interaction between PAK4 and its native binding partners.  
 CC Inhibition of PAK4 activity or expression is used for treatment of cancer  
 CC and arthritis. The present sequence represents the kinase domain fragment  
 CC of human serine/threonine kinase, PAK4  
 XX  
 SQ Sequence 250 AA;

Query Match 96.5%; Score 436; DB 3; Length 250;  
 Best Local Similarity 95.5%; Pred. No. 5.5e-48;  
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHRMNEE 60  
 DB 33 KQORELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHRMNEE 92  
 QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89  
 DB 93 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 121

RESULT 7  
 ADE15851  
 ID ADE15851 standard; protein; 293 AA.  
 XX  
 AC ADE15851;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE PAK4KD protein.  
 XX  
 KM PAK4KD protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003087816-A1.  
 XX  
 PD 23-OCT-2003.  
 XX  
 PF 08-APR-2003; 2003WO-US010878.

XX  
 PR 09-APR-2002; 2002US-0371018P.  
 PR 02-DEC-2002; 2002US-0430567P.  
 XX  
 XX (STRU-) STRUCTURAL GENOMIX INC.  
 XX  
 PI Antonyam SS, Fell I, Buchanan SG, Post KM, Liu Y, Lorber D;  
 XX  
 DR WPI; 2003-853974/79.  
 XX  
 PT Producing a computer-readable database comprising the three-dimensional  
 PT molecular structural coordinates of a binding pocket of a PAK4D protein,  
 PT comprises introducing the structural coordinates into a computer.  
 XX  
 PS Claim 17; SEQ ID NO 5; 421pp; English.  
 XX  
 CC The present invention relates to producing a computer-readable database  
 CC comprising the three-dimensional molecular structural coordinates of a  
 CC binding pocket of a PAK4D protein, comprising introducing the structural  
 CC coordinates to into a computer to produce a database containing the  
 CC molecular structural coordinates of the protein or binding pocket. The  
 CC method is useful for producing a machine-readable database for  
 CC identifying and designing inhibitors, activators and mutants of PAK4D,  
 CC PAK4D crystals and compounds or compositions that affect PAK4D  
 CC activity. The present sequence represents a primer of the invention.  
 XX  
 SQ Sequence 293 AA;

Query Match 96.5%; Score 436; DB 7; Length 293;  
 Best Local Similarity 95.5%; Pred. No. 6.9e-48;  
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHRMNEE 60  
 DB 58 KQORELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHRMNEE 117  
 QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89  
 DB 118 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 146

RESULT 8  
 AAY55941  
 ID AAY55941 standard; protein; 398 AA.  
 XX  
 AC AAY55941;  
 XX  
 DT 18-FEB-2000 (first entry)  
 XX  
 DE Human PAK5 protein.  
 XX  
 KM Antithrombotic; antithrombotic; antiinflammatory; antiallergic; osteopathic;  
 KM antiproliferative; antiarteriosclerotic; antiaesthetic; immunosuppressive;  
 KM neuroprotective; cardiac; cerebroprotective; cytostatic; antiadhesive;  
 KM vulnery; STE20; protein kinase; STIK3; STIK4; STIK5; STIK6; STIK7;  
 KM ZC1; ZC2; ZC3; ZC4; KH82; SUVU1; SUVU3; GEK2; PAK4; PAK5; antagonist;  
 KM antibody; gene therapy; rheumatoid arthritis; atherosclerosis; asthma;  
 KM inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;  
 KM rhinitis; autoimmunity; organ transplantation; multiple sclerosis;  
 KM myocardial infarction; cardiovascular disease; stroke; renal failure;  
 KM oxidative stress-related neurodegenerative disorder; Parkinson's disease;  
 KM amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;  
 KM ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;  
 KM megalgal disorder; growth regulation; wound healing; T cell activation;  
 KM immunosuppressant.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9953036-A2.  
 XX  
 PD 21-OCT-1999.  
 XX  
 PF 13-APR-1999; 99WO-US008150.



XX	PR	14-APR-1998;	98US-0081784P.
XX	PA	(SUGE-) SUGEN INC.	
XX	PI	Plowman G, Martinez R, Whyte D;	
XX	DR	WPI, 1999-611301/52.	
XX	DR	N-PSDB; AAZ40493.	
XX	PT	Novel kinase-related polypeptides used for the diagnosis and treatment of	
XX	PT	kinase-related diseases and disorders.	
XX	PS	Disclosure; Page 310-312; 387pp; English.	
XX	CC	This sequence represents a novel STE20-related protein kinase. The	
XX	CC	invention relates to nucleic acid molecule encoding a kinase polypeptide	
XX	CC	selected from STLK2, STLK3, STLK4, STK5, STLK7, ZC1, ZC2, ZC3,	
XX	CC	ZC4, KMS2, SNU1, SNU3, GEX2, PAK4 and PAK5. The proteins are used to	
XX	CC	identify agonists and antagonists, and to raise antibodies. The	
XX	CC	polynucleotides are useful in gene therapy protocols. The polynucleotides,	
XX	CC	polypeptides, antibodies, antagonists and agonists may be used to treat	
XX	CC	diseases such as immune-related disorders and diseases (e.g. rheumatoid	
XX	CC	arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g.	
XX	CC	Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,	
XX	CC	rhinitis, autoimmunity, and organ transplantation, chronic inflammatory	
XX	CC	relivic disease, multiple sclerosis, organ transplantation, myocardial	
XX	CC	infarction, cardiovascular disease, stroke, renal failure, oxidative	
XX	CC	stress-related neurodegenerative disorders (e.g. amyotrophic lateral	
XX	CC	sclerosis, Parkinson's disease and Leigh syndrome), cancer,	
XX	CC	cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes	
XX	CC	melittis, fibrotic and mesangial disorders. The proteins may also be	
XX	CC	useful for cell growth regulation (e.g. in wound healing), T cell	
XX	CC	activation, mitosis control, and as immunosuppressants	
XX	SQ	Sequence 398 AA;	
XX	Query Match	96.5%; Score 436; DB 2; Length 398;	
XX	Best Local Similarity	95.5%; Pred. No. 1, 1e-47;	
XX	Matches	85; Conservative 3; Mismatches 1; Indels 0; Gaps 0	
OY	1	KQQRRELLFNEVVIWRDYPHEVNVEMTNSYLVDGDELVVMEFEGALTDIVYHTTMMNEE	60
DB	163	KQQRRELLFNEVVIWRDYPHEVNVEMTNSYLVDGDELVVMEFEGALTDIVYHTTMMNEE	222
OY	61	OIAAVCLAVLQALVLAHQGVVHSPIKTD	89
DB	223	OIAAVCLAVLQALVLAHQGVVHSPIKTD	251
XX	RESULT 9		
XX	ADCC37305		
XX	ID	ADC37305 standard; protein; 438 AA.	
XX	AC	ADC37305;	
XX	DT	18-DEC-2003 (first entry)	
XX	DE	Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 138.	
XX	XX	Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;	
XX	XX	cancer; infectious disease; bone disease; AIDS;	
XX	XX	neurodegenerative disease; ischemic disorder; Antiinflammatory;	
XX	XX	immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;	
XX	XX	Neuroprotective; Nootropic; Cardiant; Gene therapy; human.	
XX	OS	Homo sapiens.	
XX	PN	WO2003048202-A2.	
XX	PD	12-JUN-2003.	
XX	PF	03-DEC-2002; 2002WO-JP012644.	

[illegible]

PI Mateuda A, Muramatsu S;  
 XX WPI; 2003-505282/47.  
 DR N-PSDB; AOC37308.  
 XX  
 PT New purified protein that activates nuclear factor kappa B (NF-kappaB),  
 PT useful for treating inflammation, autoimmune diseases, cancers,  
 PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or  
 PT ischemic disorders.  
 XX  
 PS Claim 1; SEQ ID NO 142; 938bp; English.  
 CC  
 CC The present invention relates to novel proteins and their coding  
 CC sequences (ADCC37168-ADCC37455), which activate nuclear factor kappa B (NF-  
 CC kappaB). The proteins and their coding sequences are useful for treating  
 CC a disease associated with NF-kappaB activation, such as inflammation,  
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,  
 CC neurodegenerative diseases, or ischemic disorders.  
 CC  
 SQ Sequence 501 AA;  
 CC  
 CC Query Match 96.5%; Score 436; DB 7; Length 501;  
 CC Best Local Similarity 95.5%; Pred. No. 1.5e-47;  
 CC Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 CC  
 QY 1 KOORRELLFNEVYIMRDYRHEVNVEMVNSYLVGDELWVMEFLGALTDIVTHTRMNEE 60  
 DB 266 KOORRELLFNEVYIMRDYRHEVNVEMVNSYLVGDELWVMEFLGALTDIVTHTRMNEE 60  
 QY 61 QIAAVCLAVLQALSVLHAQGVTHSDIKTD 89  
 DB 326 QIAAVCLAVLQALSVLHAQGVTHSDIKSD 354  
 DB  
 RESULT 11  
 ID AEM84642  
 AC AEM84642;  
 DT 18-NOV-2004 (first entry)  
 DE Human diagnostic and therapeutic protein SEQ ID NO:4891.  
 KM Gene therapy; human diagnostic and therapeutic polynucleotide; dthp.  
 OS Homo sapiens.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PF 12-SEP-2003; 2003WO-US028227.  
 PR 12-SEP-2002; 2002US-0410259P.  
 PR 12-SEP-2002; 2002US-0410260P.  
 PA (INCY-) INCYTE CORP.  
 XX  
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,  
 PI Hartschorn TA, Suchorolski MT, Altus CM, Pitts SU, Elder LV,  
 PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP,  
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH,  
 PI Peralta CH, Anderson SB, Rlouk P, Shen EJ, Wu MC, Stuve IL;  
 PI Lagace RE, Spito PA, Stewart EA, Wingrove J, Vilt UA, Kilton ES;  
 PI Xu Y, Kwong M, Policky JU, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
 PI Patury S, Shi X, Suarez CJ;  
 XX WPI; 2004-329368/30.  
 DR N-PSDB; ACN43294.  
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful  
 PT in diagnosing a condition, disease or disorder associated with human

PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
 PT in gene mapping.  
 XX  
 XX Claim 27; Page; 190pp; English.  
 PS  
 CC The invention relates to novel diagnostic and therapeutic polynucleotides  
 CC selected from one of the 2722 sequences defined in the specification. A  
 CC polynucleotide of the invention may have a use in gene therapy. The human  
 CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be  
 CC used to diagnose a particular condition, disease or disorder associated  
 CC with human molecules, e.g. cell proliferative disorders,  
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
 CC disorder, neurological disorders, gastrointestinal disorders, or  
 CC infections caused by virus, bacteria, fungi or parasite. The dthp  
 CC molecules may also be used in genetic mapping, in identifying individuals  
 CC from minute biological samples, in detecting single nucleotide  
 CC polymorphisms, as molecular weight markers, and for somatic or germline  
 CC gene therapy. The present sequence represents a dthp protein of the  
 CC invention. Note: The sequence data for this patent is not represented in  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
 CC  
 SQ Sequence 522 AA;  
 CC  
 CC Query Match 96.5%; Score 436; DB 8; Length 522;  
 CC Best Local Similarity 95.5%; Pred. No. 1.5e-47;  
 CC Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 CC  
 QY 1 KOORRELLFNEVYIMRDYRHEVNVEMVNSYLVGDELWVMEFLGALTDIVTHTRMNEE 60  
 DB 287 KOORRELLFNEVYIMRDYRHEVNVEMVNSYLVGDELWVMEFLGALTDIVTHTRMNEE 346  
 QY 61 QIAAVCLAVLQALSVLHAQGVTHSDIKTD 89  
 DB 347 QIAAVCLAVLQALSVLHAQGVTHSDIKSD 375  
 DB  
 RESULT 12  
 ID AEM84644  
 AC AEM84644;  
 DT 18-NOV-2004 (first entry)  
 DE Human diagnostic and therapeutic protein SEQ ID NO:4893.  
 KM Gene therapy; human diagnostic and therapeutic polynucleotide; dthp.  
 OS Homo sapiens.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PF 12-SEP-2003; 2003WO-US028227.  
 PR 12-SEP-2002; 2002US-0410259P.  
 PR 12-SEP-2002; 2002US-0410260P.  
 PA (INCY-) INCYTE CORP.  
 XX  
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,  
 PI Hartschorn TA, Suchorolski MT, Altus CM, Pitts SU, Elder LV,  
 PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP,  
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH,  
 PI Peralta CH, Anderson SB, Rlouk P, Shen EJ, Wu MC, Stuve IL;  
 PI Lagace RE, Spito PA, Stewart EA, Wingrove J, Vilt UA, Kilton ES;  
 PI Xu Y, Kwong M, Policky JU, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
 PI Patury S, Shi X, Suarez CJ;  
 XX WPI; 2004-329368/30.  
 DR N-PSDB; ACN43296.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
 PT in diagnosing a condition, disease or disorder associated with human  
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
 PT in gene mapping.  
 PS Claim 27; Page: 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides  
 CC selected from one of the 2722 sequences defined in the specification. A  
 CC polynucleotide of the invention may have a use in gene therapy. The human  
 CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be  
 CC used to diagnose a particular condition, disease or disorder associated  
 CC with human molecules, e.g. cell proliferative disorders,  
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
 CC disorder, neurological disorders, gastrointestinal disorders, or  
 CC infections caused by virus, bacteria, fungi or parasite. The dthp  
 CC molecules may also be used in genetic mapping, in identifying individuals  
 CC from minute biological samples, in detecting single nucleotide  
 CC polymorphisms, as molecular weight markers, and for somatic or germline  
 CC gene therapy. The present sequence represents a dthp protein of the  
 CC invention. Note: The sequence data for this patent is not represented in  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

XX Sequence 522 AA;  
 SQ

Query Match 96.5%; Score 436; DB 8; Length 522;  
 Best Local Similarity 95.5%; Pred. No. 1.5e-47;  
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOORRELLFNEVIMRDYHENVVEMVNSYLVGDELMVMEFLGGALTDIYHTRMNEE 60  
 DB 287 KOORRELLFNEVIMRDYHENVVEMVNSYLVGDELMVMEFLGGALTDIYHTRMNEE 346  
 OY 61 QIAAVCLAVLQALSVLHAQGVIRHDIKTD 89  
 DB 347 QIAAVCLAVLQALSVLHAQGVIRHDIKSD 375

RESULT 13  
 ABM84645  
 ID ABM84645 standard; protein; 522 AA.  
 AC ABM84645;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4894.  
 XX  
 KW gene therapy; human diagnostic and therapeutic polynucleotide; dthp.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004023973-A2.  
 XX  
 PD 25-MAR-2004.  
 XX  
 PF 12-SEP-2003; 2003WO-US028227.  
 XX  
 PR 12-SEP-2002; 2002US-0410259P.  
 PR 12-SEP-2002; 2002US-0410260P.  
 XX  
 PA (INCY-) INCYTE CORP.  
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,  
 PI Harshborne TA, Suchorski MT, Altus CM, Pites SJ, Eider LV,  
 PI Mooney EM, Deleagane AM, Panesar IS, Banville SC, Reddy TP,  
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH,  
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL,  
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilec UA, Kliron BE,  
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gletsen D,  
 PI Patury S, Shi X, Suarez CJ,

XX WPI; 2004-329368/30.  
 DR N-PSDB; ACN43297.  
 XX  
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
 PT in diagnosing a condition, disease or disorder associated with human  
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
 PT in gene mapping.  
 PS Claim 27; Page: 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides  
 CC selected from one of the 2722 sequences defined in the specification. A  
 CC polynucleotide of the invention may have a use in gene therapy. The human  
 CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be  
 CC used to diagnose a particular condition, disease or disorder associated  
 CC with human molecules, e.g. cell proliferative disorders,  
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
 CC disorder, neurological disorders, gastrointestinal disorders, or  
 CC infections caused by virus, bacteria, fungi or parasite. The dthp  
 CC molecules may also be used in genetic mapping, in identifying individuals  
 CC from minute biological samples, in detecting single nucleotide  
 CC polymorphisms, as molecular weight markers, and for somatic or germline  
 CC gene therapy. The present sequence represents a dthp protein of the  
 CC invention. Note: The sequence data for this patent is not represented in  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

XX Sequence 522 AA;  
 SQ

Query Match 96.5%; Score 436; DB 8; Length 522;  
 Best Local Similarity 95.5%; Pred. No. 1.5e-47;  
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOORRELLFNEVIMRDYHENVVEMVNSYLVGDELMVMEFLGGALTDIYHTRMNEE 60  
 DB 287 KOORRELLFNEVIMRDYHENVVEMVNSYLVGDELMVMEFLGGALTDIYHTRMNEE 346  
 OY 61 QIAAVCLAVLQALSVLHAQGVIRHDIKTD 89  
 DB 347 QIAAVCLAVLQALSVLHAQGVIRHDIKSD 375

RESULT 14  
 ADH23359  
 ID ADH23359 standard; protein; 588 AA.  
 AC ADH23359;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE Human p21 (CDKN1A)-activated kinase 4 (PAK4) serine/threonine kinase #1.  
 XX  
 KW human; p21 (CDKN1A)-activated kinase 4; PAK4; serine/threonine kinase;  
 KW enzyme; HIV-Tat transcriptional activity.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003186254-A1.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PF 29-APR-2002; 2002US-00134102.  
 XX  
 PR 30-DEC-1999; 99US-0173939P.  
 PR 28-DEC-2000; 2000US-00750457.  
 XX  
 PA (CELL-) CELL SIGNALING TECHNOLOGY INC.  
 XX  
 PI Melnick MB, Moritz A, Comb MJ;  
 DR WPI; 2004-130707/13.  
 DR N-PSDB; ADH23361.

XX New isolated DNA sequence encoding PAK4 serine/threonine kinase for  
PT modulating the transcriptional activity of human immunodeficiency virus-  
PT Tat protein.

PS Claim 1; SEQ ID NO 1; 47pp; English.

CC The invention relates to an isolated DNA sequence encoding p21 (CDKN1A) -  
CC activated kinase 4 (PAK4) serine/threonine kinase. The invention is  
CC useful for modulating the transcriptional activity of HIV-Tat protein.  
CC The invention provides isolated DNA and vectors encoding PAK4 and Cdc42-  
CC GEF which synergize to stimulate Tat transcriptional activity. The  
CC present sequence represents the amino acid sequence of human PAK4.  
XX

SO Sequence 588 AA;

Query Match 96.5%; Score 436; DB 8; Length 588;  
Best Local Similarity 95.5%; Pred. No. 1.8e-47;  
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQORRELLFNEVIMRDYHENVVEMVNSYLVGDELVMVMEFLGSLTDIVTHRMNEE 60

DB 356 KQORRELLFNEVIMRDYHENVVEMVNSYLVGDELVMVMEFLGSLTDIVTHRMNEE 415

OY 61 QIAAVCLAVLQALAVLHAGVTHSDIKTD 89

DB 416 QIAAVCLAVLQALAVLHAGVTHSDIKTD 444

RESULT 15

AAVS5964  
ID AAVS5964 standard; protein; 591 AA.

AC AAVS5964;

DT 18-FEB-2000 (first entry)

DE Full length human PAK5 protein.

XX  
KW Antirheumatic; antiarthritic; antiinflammatory; antiallergic; osteopathic;  
KW antipruritic; antiarteriosclerotic; antisthmatic; immunosuppressive;  
KW neuroprotective; cardiac; cerebroprotective; cytostatic; antidiabetic;  
KW vulnery; STK20, protein kinase; STK2; STK3; STK4; STK5; STK6; STK7;  
KW ZC1; ZC2; ZC3; ZC4; KHS2; STU1; STU3; GSK2; PAK4; PAK5; antagonist;  
KW antibody; gene therapy; rheumatoid arthritis; atherosclerosis; asthma;  
KW inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;  
KW rhinitis; autoimmunity; organ transplantation; multiple sclerosis;  
KW myocardial infarction; cardiovascular disease; stroke; renal failure;  
KW oxidative stress-related neurodegenerative disorder; Parkinson's disease;  
KW amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;  
KW ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;  
KW mesangial disorder; growth regulation; wound healing; T cell activation;  
KW immunosuppressant.

OS Homo sapiens.

PN WO953036-A2.

PD 21-OCT-1999.

PF 13-APR-1999; 99WO-US008150.

PR 14-APR-1998; 98US-0081784P.

PA (SUGEN) SUGEN INC.

PI Plowman G, Martinez R, Whyte D;

DR WPI; 1999-611301/52.

DR N-PSDB; AAZ40538.

PT Novel kinase-related polypeptides used for the diagnosis and treatment of  
PT kinase-related diseases and disorders.

XX Claim 11; Page 366-368; 387pp; English.

XX This sequence represents a novel STK20-related protein kinase. The  
PS invention relates to nucleic acid molecule encoding a kinase polypeptide  
CC selected from STK2, STK3, STK4, STK5, STK6, STK7, ZC1, ZC2, ZC3,  
CC ZC4, KHS2, STU1, STU3, GSK2, PAK4 and PAK5. The proteins are used to  
CC identify agonists and antagonists, and to raise antibodies. The  
CC polynucleotides are useful in gene therapy protocols. The polynucleotides,  
CC polypeptides, antibodies, antagonists and agonists may be used to treat  
CC diseases such as immune-related disorders and diseases (e.g. rheumatoid  
CC arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g.  
CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,  
CC rhinitis, autoimmunity, and organ transplantation, chronic inflammatory  
CC disease, multiple sclerosis, organ transplantation, myocardial  
CC infarction, cardiovascular disease, stroke, renal failure, oxidative  
CC stress-related neurodegenerative disorders (e.g. amyotrophic lateral  
CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,  
CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes  
CC mellitus, fibrotic and mesangial disorders. The proteins may also be  
CC useful for cell growth regulation (e.g. in wound healing), T cell  
XX activation, mitosis control, and as immunosuppressants

SO Sequence 591 AA;

Query Match 96.5%; Score 436; DB 2; Length 591;  
Best Local Similarity 95.5%; Pred. No. 1.8e-47;  
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQORRELLFNEVIMRDYHENVVEMVNSYLVGDELVMVMEFLGSLTDIVTHRMNEE 60

DB 356 KQORRELLFNEVIMRDYHENVVEMVNSYLVGDELVMVMEFLGSLTDIVTHRMNEE 415

OY 61 QIAAVCLAVLQALAVLHAGVTHSDIKTD 89

DB 416 QIAAVCLAVLQALAVLHAGVTHSDIKTD 444

Search completed: March 15, 2005, 11:26:31  
Job time : 31.6265 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2005, 11:30:37 ; Search time 24.2132 Seconds

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Title: US-10-693-367-14

Perfect score: 452  
Sequence: 1 KQORRELFNEVIMRDYRH.....LQALAVLAAGVHSIDIKTD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications AA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	452	100.0	89	US-10-693-367-14	Sequence 14, Appl
2	443	98.0	292	US-10-406-676-7	Sequence 7, Appl
3	443	98.0	292	US-10-406-676-12	Sequence 12, Appl
4	443	98.0	593	US-10-618-941-11	Sequence 11, Appl
5	436	96.5	250	US-10-693-367-3	Sequence 3, Appl
6	436	96.5	292	US-10-406-676-5	Sequence 5, Appl
7	436	96.5	292	US-10-406-676-6	Sequence 6, Appl
8	436	96.5	292	US-10-406-676-8	Sequence 8, Appl
9	436	96.5	292	US-10-406-676-9	Sequence 9, Appl
10	436	96.5	292	US-10-406-676-10	Sequence 10, Appl
11	436	96.5	293	US-10-406-676-11	Sequence 11, Appl
12	436	96.5	293	US-10-406-676-4	Sequence 4, Appl
13	436	96.5	398	US-09-291-417-30	Sequence 30, Appl

14	436	96.5	588	14	US-10-134-102-1	Sequence 1, Appl
15	436	96.5	591	10	US-09-291-417-103	Sequence 103, Appl
16	436	96.5	591	14	US-10-134-102-4	Sequence 4, Appl
17	436	96.5	591	15	US-10-394-322A-48	Sequence 48, Appl
18	436	96.5	591	15	US-10-693-367-2	Sequence 2, Appl
19	436	96.5	591	17	US-10-893-025-5	Sequence 5, Appl
20	421	93.1	292	15	US-10-406-676-15	Sequence 15, Appl
21	407	90.0	290	15	US-10-406-676-13	Sequence 13, Appl
22	407	90.0	719	14	US-10-331-095-2	Sequence 2, Appl
23	402	88.9	290	15	US-10-406-676-14	Sequence 14, Appl
24	402	88.9	290	15	US-10-406-676-16	Sequence 16, Appl
25	402	88.9	290	15	US-10-406-676-17	Sequence 17, Appl
26	402	88.9	580	15	US-10-108-260A-3288	Sequence 3288, Appl
27	402	88.9	719	15	US-10-331-095-4	Sequence 4, Appl
28	402	88.9	719	15	US-10-394-322A-49	Sequence 49, Appl
29	379	83.8	292	15	US-10-406-676-21	Sequence 21, Appl
30	379	83.8	641	15	US-10-311-034-15	Sequence 15, Appl
31	379	83.8	681	10	US-09-291-417-29	Sequence 29, Appl
32	376	83.2	681	10	US-09-765-815-2	Sequence 2, Appl
33	366	81.0	290	15	US-10-406-676-18	Sequence 18, Appl
34	366	81.0	290	15	US-10-406-676-19	Sequence 19, Appl
35	366	81.0	290	15	US-10-406-676-20	Sequence 20, Appl
36	366	81.0	635	14	US-10-134-102-2	Sequence 2, Appl
37	366	81.0	639	14	US-10-134-102-6	Sequence 6, Appl
38	303	67.0	542	15	US-10-369-493-6482	Sequence 6482, Appl
39	303	67.0	542	15	US-10-369-493-6483	Sequence 6483, Appl
40	283	62.6	704	15	US-10-267-502-378	Sequence 378, Appl
41	277	61.3	297	16	US-10-664-421-34	Sequence 34, Appl
42	277	61.3	305	10	US-09-765-815-10	Sequence 10, Appl
43	277	61.3	326	16	US-10-664-421-48	Sequence 48, Appl
44	277	61.3	545	9	US-09-967-624-5	Sequence 5, Appl
45	277	61.3	545	15	US-10-394-322A-45	Sequence 45, Appl

## ALIGNMENTS

RESULT 1						
US-10-693-367-14						
Sequence 14, Application US/10693367						
Publication No. US20040091992A1						
GENERAL INFORMATION:						
APPLICANT: The Trustees of Columbia University						
APPLICANT: Minden, Audrey						
TITLE OF INVENTION: PAR4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE						
FILE REFERENCE: 575/5511-A-PCT-US						
CURRENT FILING DATE: 2003-10-24						
PRIOR APPLICATION NUMBER: US/09/718, 032						
PRIOR FILING DATE: 2000-11-21						
PRIOR APPLICATION NUMBER: PCT/US99/11341						
PRIOR FILING DATE: 1999-05-21						
PRIOR APPLICATION NUMBER: 09/082,737						
PRIOR FILING DATE: 1998-05-21						
NUMBER OF SEQ ID NOS: 17						
SOFTWARE: PatentIn version 3.1						
SEQ ID NO 14						
LENGTH: 89						
TYPE: PRT						
ORGANISM: mouse						
US-10-693-367-14						
Query Match						
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Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
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DB	1	KQORRELFNEVIMRDYRHENVYNNYSYLVGDELAVVMEFLGGALTDIVHTPMNE	60			
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DB	61	QIAAVCLAVLQALAVLAAGVHSIDIKTD	89			

## RESULT 2

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US-10-406-676-7
; Sequence 7, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonyamy, Stephen
; APPLICANT: Fell, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 292
; TYPE: PRT
; ORGANISM: M. musculus
US-10-406-676-7
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Best Local Similarity 97.8%; Pred. No. 3.8e-40;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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DB 57 KQORELLFNEVIMRDYRHENVEMVNSYVGDLELWVMEFLGALTDIVTHTRMNEE 116
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DB 117 QIAAVCLAVLQALAVLHAQGVTHSDIKSD 145
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## RESULT 3

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US-10-406-676-12
; Sequence 12, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonyamy, Stephen
; APPLICANT: Fell, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
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; TYPE: PRT
; ORGANISM: M. musculus
US-10-406-676-12
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Query Match          98.0%; Score 443; DB 15; Length 292;
Best Local Similarity 97.8%; Pred. No. 3.8e-40;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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DB 57 KQORELLFNEVIMRDYRHENVEMVNSYVGDLELWVMEFLGALTDIVTHTRMNEE 116
    |||
DB 117 QIAAVCLAVLQALAVLHAQGVTHSDIKSD 145
    |||
```

## RESULT 4

```
US-10-618-941-111
; Sequence 111, Application US/10618941
; Publication No. US2004019792A1
; GENERAL INFORMATION:
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERRARD
; APPLICANT: CAENEPEL, SEAN
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-0321
; CURRENT APPLICATION NUMBER: US/10/618,941
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/395,632
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-618-941-111
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Query Match          98.0%; Score 443; DB 16; Length 593;
Best Local Similarity 97.8%; Pred. No. 8.5e-40;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 KQORELLFNEVIMRDYRHENVEMVNSYVGDLELWVMEFLGALTDIVTHTRMNEE 60
    |||
DB 358 KQORELLFNEVIMRDYRHENVEMVNSYVGDLELWVMEFLGALTDIVTHTRMNEE 417
    |||
DB 418 QIAAVCLAVLQALAVLHAQGVTHSDIKSD 446
    |||
```

## RESULT 5

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US-10-693-367-3
; Sequence 3, Application US/10693367
; Publication No. US20040091992A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
; FILE REFERENCE: 575/55311-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/693,367
; CURRENT FILING DATE: 2003-10-24
; PRIOR APPLICATION NUMBER: US/09/718,032
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: PCT/US99/11341
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 09/082,737
; PRIOR FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 250
; TYPE: PRT
; ORGANISM: human
US-10-693-367-3
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Query Match          96.5%; Score 436; DB 15; Length 250;
Best Local Similarity 95.5%; Pred. No. 1.8e-39;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHTRMNEE 60
    |||||
DB 33 KOORRELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHTRMNEE 92
    |||||

QY 61 QIAAVCLAVLQALSVLHAQGVTHSDIKTD 89
    |||||
DB 93 QIAAVCLAVLQALSVLHAQGVTHSDIKTD 121
    |||||

RESULT 6
US-10-406-676-5
; Sequence 5, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Anthonyamy, Stephen
; APPLICANT: Fell, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-676-5

Query Match          96.5%; Score 436; DB 15; Length 292;
Best Local Similarity 95.5%; Pred. No. 2.2e-39;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHTRMNEE 60
    |||||
DB 57 KOORRELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHTRMNEE 116
    |||||

QY 61 QIAAVCLAVLQALSVLHAQGVTHSDIKTD 89
    |||||
DB 117 QIAAVCLAVLQALSVLHAQGVTHSDIKTD 145
    |||||

RESULT 7
US-10-406-676-6
; Sequence 6, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Anthonyamy, Stephen
; APPLICANT: Fell, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-676-6
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; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-676-6

Query Match          96.5%; Score 436; DB 15; Length 292;
Best Local Similarity 95.5%; Pred. No. 2.2e-39;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHTRMNEE 60
    |||||
DB 57 KOORRELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHTRMNEE 116
    |||||

QY 61 QIAAVCLAVLQALSVLHAQGVTHSDIKTD 89
    |||||
DB 117 QIAAVCLAVLQALSVLHAQGVTHSDIKTD 145
    |||||

RESULT 8
US-10-406-676-8
; Sequence 8, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Anthonyamy, Stephen
; APPLICANT: Fell, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 292
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-406-676-8

Query Match          96.5%; Score 436; DB 15; Length 292;
Best Local Similarity 95.5%; Pred. No. 2.2e-39;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHTRMNEE 60
    |||||
DB 57 KOORRELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHTRMNEE 116
    |||||

QY 61 QIAAVCLAVLQALSVLHAQGVTHSDIKTD 89
    |||||
DB 117 QIAAVCLAVLQALSVLHAQGVTHSDIKTD 145
    |||||

RESULT 9
US-10-406-676-9
; Sequence 9, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Anthonyamy, Stephen
; APPLICANT: Fell, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-676-9
```

```
/ APPLICANT: Fell, Ingeborg
/ APPLICANT: Buchanan, Sean
/ APPLICANT: Post, Kai W.
/ APPLICANT: Liu, Yi
/ APPLICANT: Lorber, David
/ TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
/ FILE REFERENCE: 524982002300
/ CURRENT APPLICATION NUMBER: US/10/406,676
/ PRIOR FILING DATE: 2003-04-02
/ PRIOR APPLICATION NUMBER: 60/371,018
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/430,567
/ PRIOR FILING DATE: 2002-12-02
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 292
/ TYPE: PRT
/ ORGANISM: H. sapiens
US-10-406-676-9

Query Match          96.5%; Score 436; DB 15; Length 292;
Best Local Similarity 95.5%; Pred. No. 2.2e-39;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELFENEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 60
DB 57 KOORRELFENEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 116
DB 117 QIAAVCLAVLQALSVLHAQGVTHRDIKSD 145

RESULT 10
US-10-406-676-10
/ Sequence 10, Application US/10406676
/ Publication No. US20030229453A1
/ GENERAL INFORMATION:
/ APPLICANT: Structural Genomix, Inc.
/ APPLICANT: Antonyasamy, Stephen
/ APPLICANT: Fell, Ingeborg
/ APPLICANT: Buchanan, Sean
/ APPLICANT: Post, Kai W.
/ APPLICANT: Liu, Yi
/ APPLICANT: Lorber, David
/ TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
/ FILE REFERENCE: 524982002300
/ CURRENT APPLICATION NUMBER: US/10/406,676
/ CURRENT FILING DATE: 2003-04-02
/ PRIOR APPLICATION NUMBER: 60/371,018
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/430,567
/ PRIOR FILING DATE: 2002-12-02
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10
/ LENGTH: 292
/ TYPE: PRT
/ ORGANISM: H. sapiens
US-10-406-676-10

Query Match          96.5%; Score 436; DB 15; Length 292;
Best Local Similarity 95.5%; Pred. No. 2.2e-39;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELFENEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 60
DB 57 KOORRELFENEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 116
DB 117 QIAAVCLAVLQALSVLHAQGVTHRDIKSD 145
```

```
DB 117 QIAAVCLAVLQALSVLHAQGVTHRDIKSD 145

RESULT 11
US-10-406-676-11
/ Sequence 11, Application US/10406676
/ Publication No. US20030229453A1
/ GENERAL INFORMATION:
/ APPLICANT: Structural Genomix, Inc.
/ APPLICANT: Antonyasamy, Stephen
/ APPLICANT: Fell, Ingeborg
/ APPLICANT: Buchanan, Sean
/ APPLICANT: Post, Kai W.
/ APPLICANT: Liu, Yi
/ APPLICANT: Lorber, David
/ TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
/ FILE REFERENCE: 524982002300
/ CURRENT APPLICATION NUMBER: US/10/406,676
/ CURRENT FILING DATE: 2003-04-02
/ PRIOR APPLICATION NUMBER: 60/371,018
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/430,567
/ PRIOR FILING DATE: 2002-12-02
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 11
/ LENGTH: 292
/ TYPE: PRT
/ ORGANISM: H. sapiens
US-10-406-676-11

Query Match          96.5%; Score 436; DB 15; Length 292;
Best Local Similarity 95.5%; Pred. No. 2.2e-39;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELFENEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 60
DB 57 KOORRELFENEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 116
DB 117 QIAAVCLAVLQALSVLHAQGVTHRDIKSD 145

RESULT 12
US-10-406-676-12
/ Sequence 12, Application US/10406676
/ Publication No. US20030229453A1
/ GENERAL INFORMATION:
/ APPLICANT: Structural Genomix, Inc.
/ APPLICANT: Antonyasamy, Stephen
/ APPLICANT: Fell, Ingeborg
/ APPLICANT: Buchanan, Sean
/ APPLICANT: Post, Kai W.
/ APPLICANT: Liu, Yi
/ APPLICANT: Lorber, David
/ TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
/ FILE REFERENCE: 524982002300
/ CURRENT APPLICATION NUMBER: US/10/406,676
/ CURRENT FILING DATE: 2003-04-02
/ PRIOR APPLICATION NUMBER: 60/371,018
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/430,567
/ PRIOR FILING DATE: 2002-12-02
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12
/ LENGTH: 293
/ TYPE: PRT
/ ORGANISM: Homo sapiens
```



US-10-406-676-4

Query Match 96.5%; Score 436; DB 15; Length 293;  
Best Local Similarity 95.5%; Pred. No. 2,2e-39;  
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVYIMRDYHENVVEMVNSYLVGDELMVMEFLGGALTDIVHTRMNEE 60  
DB 58 KOORRELLFNEVYIMRDYHENVVEMVNSYLVGDELMVMEFLGGALTDIVHTRMNEE 117

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89  
DB 118 QIAAVCLAVLQALSVLHAQGVHSDIKSD 146

RESULT 13  
US-09-291-417-30  
; Sequence 30, Application US/09291417A  
; Publication No. US20030050230A1  
; GENERAL INFORMATION:  
; APPLICANT: PLOMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHYTE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 240/300  
; CURRENT APPLICATION NUMBER: US/09/291,417A  
; CURRENT FILING DATE: 1999-04-13  
; EARLIER APPLICATION NUMBER: US 60/081,784  
; EARLIER FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 30  
; LENGTH: 398  
; TYPE: PRT  
; ORGANISM: Mammalian (Human) PAK5  
US-09-291-417-30

Query Match 96.5%; Score 436; DB 10; Length 398;  
Best Local Similarity 95.5%; Pred. No. 3.1e-39;  
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVYIMRDYHENVVEMVNSYLVGDELMVMEFLGGALTDIVHTRMNEE 60  
DB 163 KOORRELLFNEVYIMRDYHENVVEMVNSYLVGDELMVMEFLGGALTDIVHTRMNEE 222

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89  
DB 223 QIAAVCLAVLQALSVLHAQGVHSDIKSD 251

RESULT 14  
US-10-134-102-1  
; Sequence 1, Application US/10134102  
; Publication No. US20030186254A1  
; GENERAL INFORMATION:  
; APPLICANT: Melnick, Michael B.  
; APPLICANT: Moritz, Albrecht  
; APPLICANT: Comb, Michael J.  
; TITLE OF INVENTION: Regulation of HIV-Tat and Nef by the Pak4 kinase and its  
; FILE REFERENCE: CST-176 CIP  
; CURRENT APPLICATION NUMBER: US/10/134,102  
; CURRENT FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: 09/750,457  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: 60/173,939  
; PRIOR FILING DATE: 1999-12-30  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 588  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-134-102-1

Query Match 96.5%; Score 436; DB 14; Length 588;  
Best Local Similarity 95.5%; Pred. No. 4.9e-39;  
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVYIMRDYHENVVEMVNSYLVGDELMVMEFLGGALTDIVHTRMNEE 60  
DB 356 KOORRELLFNEVYIMRDYHENVVEMVNSYLVGDELMVMEFLGGALTDIVHTRMNEE 415

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89  
DB 416 QIAAVCLAVLQALSVLHAQGVHSDIKSD 444

RESULT 15  
US-09-291-417-103  
; Sequence 103, Application US/09291417A  
; Publication No. US20030050230A1  
; GENERAL INFORMATION:  
; APPLICANT: PLOMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHYTE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 240/300  
; CURRENT APPLICATION NUMBER: US/09/291,417A  
; CURRENT FILING DATE: 1999-04-13  
; EARLIER APPLICATION NUMBER: US 60/081,784  
; EARLIER FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 103  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Full Length Mammalian (Human) PAK5hu  
US-09-291-417-103

Query Match 96.5%; Score 436; DB 10; Length 591;  
Best Local Similarity 95.5%; Pred. No. 4.9e-39;  
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVYIMRDYHENVVEMVNSYLVGDELMVMEFLGGALTDIVHTRMNEE 60  
DB 356 KOORRELLFNEVYIMRDYHENVVEMVNSYLVGDELMVMEFLGGALTDIVHTRMNEE 415

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89  
DB 416 QIAAVCLAVLQALSVLHAQGVHSDIKSD 444

Search completed: March 15, 2005, 11:48:06  
Job time : 32.2132 secs

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```
COUNTRY: U.S.A.
ZIP: 11230
COMPUTER READABLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,737
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/55311
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-082-737-3
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Query Match          96.5%; Score 436; DB 3; Length 250;
Best Local Similarity 95.5%; Pred. No. 1e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 KOORRELFNEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 60
    |||
DB 3 KOORRELFNEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 92
QY 61 QIAAVCLAVLQALSVLHAQGVHSIDIKTD 89
    |||
DB 93 QIAAVCLAVLQALSVLHAQGVHSIDIKTD 121
```

```
RESULT 3
US-09-718-032-3
; Sequence 3, Application US/09718032
; Patent No. 6667168
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PARK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
; FILE REFERENCE: 575/55311-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/718,032
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: PCT/US99/11341
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 09/082,737
; PRIOR FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 250
; TYPE: PRT
; ORGANISM: human
US-09-718-032-3
```

```
Query Match          96.5%; Score 436; DB 4; Length 250;
Best Local Similarity 95.5%; Pred. No. 1e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KOORRELFNEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 60
    |||
DB 3 KOORRELFNEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 92
QY 61 QIAAVCLAVLQALSVLHAQGVHSIDIKTD 89
    |||
```

```
DB 93 QIAAVCLAVLQALSVLHAQGVHSIDIKSD 121
```

```
RESULT 4
US-09-688-188B-30
; Sequence 30, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-188B-30
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```
Query Match          96.5%; Score 436; DB 4; Length 398;
Best Local Similarity 95.5%; Pred. No. 2e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KOORRELFNEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 60
    |||
DB 163 KOORRELFNEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 222
QY 61 QIAAVCLAVLQALSVLHAQGVHSIDIKTD 89
    |||
DB 223 QIAAVCLAVLQALSVLHAQGVHSIDIKSD 251
```

```
RESULT 5
US-09-291-417D-30
; Sequence 30, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-30
```

```
Query Match          96.5%; Score 436; DB 4; Length 398;
Best Local Similarity 95.5%; Pred. No. 2e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KOORRELFNEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 60
    |||
DB 163 KOORRELFNEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 222
QY 61 QIAAVCLAVLQALSVLHAQGVHSIDIKTD 89
    |||
DB 223 QIAAVCLAVLQALSVLHAQGVHSIDIKSD 251
```

```

; SEQ ID NO 103
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-1888-103

Query Match
Best Local Similarity 96.5%; Score 436; DB 4; Length 591;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0

Cy 1 KQORRELLFNEVWIRDRYHENVVMYNSYLVGDELMVMEFLGGALTDIVYHTMNEE 60
Db 356 KQORRELLFNEVWIRDRYQHEHVVEMVNSYLVGDELMVMEFLGGALTDIVYHTMNEE 415
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 QIAAVCLAVLQALAVLHAQGVYHSDIKTD 89
Db 416 QIAAVCLAVLQALAVLHAQGVYHRIKSD 444
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
US-09-718-032-2
; Sequence 2, Application US/09718032
; Patent No. 6667168
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
; FILE REFERENCE: 575/55311-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/718,032
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: PCT/US99/11341
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 09/082,737
; PRIOR FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 591
; TYPE: PRT
; ORGANISM: human
US-09-718-032-2

Query Match
Best Local Similarity 96.5%; Score 436; DB 4; Length 591;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0

Cy 1 KQORRELLFNEVWIRDRYHENVVMYNSYLVGDELMVMEFLGGALTDIVYHTMNEE 60
Db 356 KQORRELLFNEVWIRDRYQHEHVVEMVNSYLVGDELMVMEFLGGALTDIVYHTMNEE 415
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 QIAAVCLAVLQALAVLHAQGVYHSDIKTD 89
Db 416 QIAAVCLAVLQALAVLHAQGVYHRIKSD 444
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
US-09-291-417D-103
; Sequence 103, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 103
; LENGTH: 591

```

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 29  
LENGTH: 681  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-291-417D-29

Query Match  
Best Local Similarity 83.8%; Score 379; DB 4; Length 681;  
Best Local Similarity 83.1%; Pred. No. 8, 2e-40;  
Matches 74; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 KOQRELLFNEVYINRDYRHENVEMVNSYLVGDELWVMEFLGEGALTDIVYTHRMNEE 60  
DB 442 KOQRELLFNEVYINRDYQHFNVEVMYKSYLVGEBLWVMEFLGEGALTDIVSQRVLRNEE 501  
QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89  
DB 502 QIATVCEAVLQALAVLHAQGVTHSDIKSD 530

## RESULT 14

US-09-949-016-10445  
Sequence 10445, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CLO01307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10445  
LENGTH: 694  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-10445

Query Match  
Best Local Similarity 83.8%; Score 379; DB 4; Length 694;  
Best Local Similarity 83.1%; Pred. No. 8, 4e-40;  
Matches 74; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 KOQRELLFNEVYINRDYRHENVEMVNSYLVGDELWVMEFLGEGALTDIVYTHRMNEE 60  
DB 455 KOQRELLFNEVYINRDYQHFNVEVMYKSYLVGEBLWVMEFLGEGALTDIVSQRVLRNEE 514  
QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89  
DB 515 QIATVCEAVLQALAVLHAQGVTHSDIKSD 543

## RESULT 15

US-09-765-815-2  
Sequence 2, Application US/09765815  
Patent No. 6673586  
GENERAL INFORMATION:  
APPLICANT: Baik, Steven  
TITLE OF INVENTION: No. 6673586e1 Steroid Hormone Receptor  
FILE REFERENCE: 01948/068002  
CURRENT APPLICATION NUMBER: US/09/765,815  
CURRENT FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: US 60/176,859  
PRIOR FILING DATE: 2000-01-19  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2

LENGTH: 681  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-765-815-2

Query Match  
Best Local Similarity 83.2%; Score 376; DB 4; Length 681;  
Best Local Similarity 82.0%; Pred. No. 2e-39;  
Matches 73; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 KOQRELLFNEVYINRDYRHENVEMVNSYLVGDELWVMEFLGEGALTDIVYTHRMNEE 60  
DB 442 KOQRELLFNEVYINRDYQHFNVEVMYKSYLVGEBLWVMEFLGEGALTDIVSQRVLRNEE 501  
QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89  
DB 502 QIATVCEAVLQALAVLHAQGVTHSDIKSD 530

Search completed: March 15, 2005, 11:32:29  
Job time : 7.85294 secs

*This Page Blank (uspto)*



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2005, 11:16:56 ; Search time 44.325 Seconds

(Without alignments)  
1282.890 Million cell updates/sec

Title: US-10-693-367-2

Perfect score: 3090  
Sequence: 1 MGCKKKRVEISAPSNFEHR.....LAKGPPASIVPLMRQNR 591

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1096.5	35.5	540	2	T19956	hypothetical prote
2	1090.5	35.3	542	2	T19952	hypothetical prote
3	917	29.7	544	2	A57597	beta-p21-activated
4	907	29.4	544	2	T149376	p21 activated kina
5	895.5	29.0	525	2	S58682	protein kinase, p2
6	892.5	28.9	545	2	G01773	p21-activated prot
7	892	28.9	544	2	S40482	serine/threonine-s
8	846.5	27.4	1230	2	T18256	probable serine/th
9	846.5	27.4	1230	2	T18259	serine/threonine p
10	837	27.1	939	2	S28394	probable serine/th
11	823.5	26.7	658	2	T39500	serine/threonine-s
12	814.5	26.4	658	2	S60170	protein kinase Pak
13	811.5	26.3	622	2	T15467	hypothetical prote
14	760	24.6	842	2	S60402	protein kinase CLA
15	722	23.4	378	2	T26684	hypothetical prote
16	697	22.6	589	2	T38086	serine/threonine-p
17	651.5	21.1	655	2	S51884	probable protein k
18	505	16.3	836	2	B96716	probable serine/th
19	498	16.1	471	2	T39232	probable serine th
20	494	16.0	1102	2	UC6316	hypothetical prote
21	478	15.5	653	2	T34356	hypothetical prote
22	476	15.4	819	2	A53714	protein kinase (EC
23	470.5	15.2	829	2	T29372	hypothetical prote
24	464	15.0	426	2	S71886	Ste20-like protein
25	463	15.0	1231	2	T18532	serine/threonine pr
26	462	15.0	1233	2	T14157	serine/threonine p
27	460	14.9	1206	2	T34021	protein kinase SK2
28	458.5	14.8	690	2	C96572	protein F12M16.4 l
29	455.5	14.7	1080	2	S48944	hypothetical prote

30	455	14.7	1233	2	T30989	serine/threonine p
31	450.5	14.6	312	2	T38525	serine/threonine p
32	444.5	14.4	1001	2	T17365	serine/threonine p
33	440.5	14.3	1075	2	T27623	hypothetical prote
34	440.5	14.3	1080	2	T27622	hypothetical prote
35	437.5	14.2	1062	2	S46367	protein kinase CDC
36	428	13.9	1228	2	T18897	hypothetical prote
37	424.5	13.7	659	1	A39723	protein kinase byr
38	421	13.6	553	2	T01479	hypothetical prote
39	419	13.6	883	2	A96662	hypothetical prote
40	417.5	13.5	1174	2	T43051	protein kinase C (
41	413	13.4	561	2	T51417	protein kinase-lik
42	409.5	13.3	652	2	T39722	serine/threonine p
43	409	13.2	891	2	T40503	protein kinase kin
44	405.5	13.1	1139	1	S61918	protein kinase C (
45	404.5	13.1	1135	1	A29813	132K nlnac protein

#### ALIGNMENTS

##### RESULT 1

T19956

hypothetical protein C45B11.1b - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #ext\_change 16-Aug-2004

C:Accession: T19956

R/McMurray, A.

A:Reference number: Z19202

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Accession: T19956

A:Molecule type: DNA

A:Residues: 1-540 <MIL>

A:Cross-references: UNIPROT:Q9U3M1; EMBL:Z74029; PIDN:CAA98433.1; GSPDB:GN00023; CESP:C

A:Experimental source: clone C45B11

C:Genetics:

A:Gene: CESP:C45B11.1b

A:Map position: 5

A:Insertions: 13/2; 62/3; 104/2; 231/3; 367/2; 468/3

C:Superfamily: protein kinase homology

Query Match	Score	Length	DB 2	Length	540;
Best Local Similarity	41.7%	Pred. No. 4.1e-31;	Matches 251;	Conservative 67;	Mismatches 151;
Indels 133;	Gaps 9;				
QY	4	KKKRVEISAPSNFEHRVHTGFDOHEOKFTGLPRQWQSLI--EESARRKPLVDPACITS	61		
DB	29	RKKKSEISTPSNFEHRHAGFDARSGTYTGLPKQWQALLGPPRSISRKPMVDPSCITP	88		
QY	62	IQGADKTVKSGKAGDALTLTLDDEFENMSVTRNSLRDSPPPPARARQENGMEEP	121		
DB	89	VDAELKTVIRGSSSYNSPLPFGMTNSPMPVSARSNSIRISATSP-----	135		
QY	122	ATTARCGPKAGSRGFAHSEACGGSGDRRAAGPEPKRSREGSGPQESSRDRPLPS	181		
DB	136	-----VVNVSARHSRFPPLPVSPQ-----	156		
QY	182	GPVGTTPQAGLASGAKLAGRPFTYPRADTDHPSRGAQGBPHDVAPNGSAGLAIHQ	241		
DB	157	-----GYPF-----NDPSYAPLPL--	170		
QY	242	SSSSSRPPTRRAGAPSPVLAGPH-----ASEPOLAPACTPAAPAVGPPG	288		
DB	171	---RNQKPPM---STTFGEKPHYOQIITTVASRTTTPOLQPKS-----PST	213		
QY	289	PSAPQREP---QVSHSEGFRAALQLVVDGDSRYDNIKIGEGSTGIVCIATVRSQK	345		
DB	214	PQMRQQPKCTGVSDEFRNALKFVVDGTDPSDITLTKQIGEGTGVEAAYKISTIKQ	273		
QY	346	LVAVKMDLRKQQRRLTFNEVYIMKDYHENVVEMVNSYLVGDELVMVMEFLGGALTD	405		
DB	274	IYAVKRMNLKQQRRLTFNEVSIIRQYQHPNIVRFFSSHVLVDDELVMVMEFLGGSLTD	333		

```
QY 406 IYTHIRMEQIATVAVCLATLQALSVTHAGQVTHRDIKSDSIILLTHDGRVKLSDFGFCQAY 465
DB 334 IYATRTMTBPQIATISRQVLGALDFLHARKVTHRDIKSDSIILLKRDGVTKLDFGFCQGL 393
QY 466 SKEVPRKSLVGTPTWMAPELISRLPYGPEVDIWSIGIWIEMVDEGPEPYFNEPPLKAMK 525
DB 394 SEEVPRRSRLVGTPTWTAETAVIAREPYDTRADIMSGCIVLIMVDEGPEPYFNDQFQAMK 453
QY 526 MIRDLNLPRLKHLKVPSPSLKGFLLDRLLVDRPAQATAAELLKHPLAKAGPPASIVPLM 585
DB 454 RIRDEHEARFBRHAKVSELSSELISHCIVDVNKRWPADLRLRHPFAKQHSSTIAPLL 513
QY 586 RQ 587
DB 514 LQ 515
```

## RESULT 2

T19952

hypothetical protein C45B11.1a - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 16-Aug-2004

C/Accession: T19952

R:McMurray, A.

submitted to the EMBL Data Library, June 1996

A/Reference number: Z19202

A/Accession: T19952

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-542 &lt;WIL&gt;

A/Cross-references: UNIPROT:Q18637; EMBL:Z74029; PIDN:CAA98429.1; GSPDB:GN00023; CESP:C4

A/Experimental source: clone C45B11

C/Genetics:

A/Map position: 5

A/Intons: 13/2; 104/2; 233/3; 369/2; 470/3

C/Superfamily: protein kinase homology

Query Match 35.3%; Score 1090.5; DB 2; Length 542;

Best Local Similarity 42.0%; Pred. No. 6,6e-31;

Matches 253; Conservative 69; Mismatches 149; Indels 131; Gaps 11;

```
QY 4 KRKKRVEISAPSNFHRVHTGPDQHQKFTGLPRQMSLI--ESARRPKPLVDPACTIS 61
DB 29 RKVKSEISLTPSFEHRIHAGFDARSGTYTGLPKQALGPPRSISRKEMWDSECTIP 88
QY 62 IOPGAKTIVRSGKAGKDGALTLTLDDEFENMSTRNSLRRDSPPPAPARQENGMPREP 121
DB 89 VDVAEIKTYLRGP-----SSFRVNSPLP-----FGMTNSP 119
QY 122 ATTARGGPGKAGRGPRFAGHSEAGSGGDRRRRAGPEKRPKSSRSGSGGFQOESSRDKRPLS 181
DB 120 MPESV---ARSNLRSATASPVVNVSSARHSFRPLPVSQR----- 158
QY 182 GPDVGTTPQAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEPHDVAAPNGPSAGLAIPO 241
DB 159 -----GYFP-----NDPSIAPLPL-- 172
QY 242 SSSSSSRPPTRAGAPSPVTLGPH-----ASBPQLAPACTPAAPAVGPPG 288
DB 173 ---RNQKPRM---STTFGEKPHQYQOQITTIIVAPRTTTPQIQPKS-----PST 215
QY 289 PRSPQREP---QVSHQGFPAALQLVDPEDPRSITLNFIKIGSGTGIVCIATVRSQK 345
DB 216 PQAMROQPKCTEGSVSEEFRNALKFVVDGTPRSDLTLDYKQIGEGSGTVGEAAVYKSTIQ 275
QY 346 LVAVKMDLRKQORRELLFNEVVIWIRDOYHENVVEMVNSYLVGDELAVVMEFLREGALND 405
DB 276 IVAVKRNLRKQORRELLFNEVSIILROYQHPNTVRFSSSHLVVDDELAVVMEFEGGSLTD 335
QY 406 IVYHTMNEEQIATVAVCLATLQALSVTHAGQVTHRDIKSDSIILLTHDGRVKLSDFGFCQAY 465
```

```
DB 336 IYATRTMTBPQIATISRQVLGALDFLHARKVTHRDIKSDSIILLKRDGVTKLDFGFCQGL 395
QY 466 SKEVPRKSLVGTPTWMAPELISRLPYGPEVDIWSIGIWIEMVDEGPEPYFNEPPLKAMK 525
DB 394 SEEVPRRSRLVGTPTWTAETAVIAREPYDTRADIMSGCIVLIMVDEGPEPYFNDQFQAMK 455
QY 526 MIRDLNLPRLKHLKVPSPSLKGFLLDRLLVDRPAQATAAELLKHPLAKAGPPASIVPLM 585
DB 454 RIRDEHEARFBRHAKVSELSSELISHCIVDVNKRWPADLRLRHPFAKQHSSTIAPLL 515
QY 586 RQ 587
DB 516 LQ 517
```

## RESULT 3

A57597

beta-p21-activated protein kinase - rat

N/Alternate names: beta-PAK

C/Species: Rattus norvegicus (Norway rat)

C/Date: 08-Feb-1996 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004

C/Accession: A57597

R/Masner, E.; Chong, C.; Zhao, Z.S.; Leung, T.; Michael, G.; Hall, C.; Lim, L.

J. Biol. Chem. 270, 25070-25078, 1995

A/Title: Molecular cloning of a new member of the p21-Cdc42/Rac-activated kinase (PAK)

A/Reference number: A57597; MUID:96027610; PMID:7559638

A/Accession: A57597

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-544 &lt;MAN&gt;

A/Cross-references: UNIPROT:Q62829; GB:U33314; NID:91039424; PIDN:AAC52268.1; PID:910394

C/Superfamily: unaassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc

C/Keywords: ATP

F/266-518/Domain: protein kinase homology &lt;KIN&gt;

F/274-282/Region: protein kinase ATP-binding motif

Query Match 29.7%; Score 917; DB 2; Length 544;

Best Local Similarity 35.8%; Pred. No. 5,2e-25;

Matches 211; Conservative 87; Mismatches 165; Indels 126; Gaps 8;

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QY 4 KRKKRVEISAPSNFHRVHTGPDQHQKFTGLPRQMSLI-----ESARRPKPLVDP 56
DB 63 KEKERPEISLSPDFEHTIHGVFDVNTGEFTGIPQWARTLQTSNITKLEQKNQAVLD- 121
QY 57 ACTISIQGAKTIVRSGKAGKDGALTLTLDDEFENMSTRNSLRRDSPPPAPARQENG 116
DB 122 -----VLKFTYSKEIVNNQKMSFT----- 141
QY 117 MPREPATTARAGPGKAGRGPRFAGHSEAGSGGDRRRRAGPEKRPKSSRSGSGGFQOESSRD 176
DB 142 -----SGDKSAHGYIAAHQ-----SNTKTASEPPLAPVSEDEDEEBEEDD 184
QY 177 KRPLSGPDVGTTPQAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEPHDVAAPNGPSAG 236
DB 185 NEP---PVIAPRPETHS-----IYTSVVSISASP-----APNKEATRP 223
QY 227 LAIPQSSSSSRPPTRAGAPSPVTLGPHASEPQLAPACTPAAPAVGPPGSPQREP 296
DB 224 SLENANSTLYRNDR-----QKK 243
QY 297 QVSHQGFPAALQLVDPEDPRSITLNFIKIGSGTGIVCIATVRSQKLVAVKMDLRK 356
DB 244 SKMTDEBELLEKRSIVSVGDPRKVTREPKIQGASGVYVYALDIATQGEVAILQMNLDQ 303
QY 357 QQRRELLFNEVVIWIRDOYHENVVEMVNSYLVGDELAVVMEFLREGALNDIYTHIRMEQ 416
DB 304 QPKKELIINEILIVMENKPNIVNYLDSYLVGDELAVVMEFLAGSLTDVVTETCMDSQ 363
QY 417 IAAVCLATLQALSVTHAGQVTHRDIKSDSIILLTHDGRVKLSDFGFCQAYVSKVPRKSLV 476
DB 364 IAAVRECEQLALDFHSHQVTHRDIKSDSIILLGMDSGYKLDVDFGCAQITTEQSGSRSTMV 423
QY 477 GTPYMAPELISRLPYGPEVDIWSIGIWIEMVDEGPEPYFNEPPLKAMKMIKMDLNLPRLK 536
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Db 424 GTPYMAPEVYTRKAGPVDIWSLGIIMAEWEGSPVLTNEMPAALVLIATNGPPEIQ 483

Qy 537 NHHKVSPLSKGLFDLLVDRPAQRATPAELIKHPFLAKAGPPASIVPLM 585  
Db 484 NPERLSAVPRDFLNRCLTENDVDRSGSAKELQHPPFLKAKPLSLPLI 532

## RESULT 4

P21 activated kinase-3 - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Aug-2004  
C/Accession: I49376  
R:Bagrodia, S.; Taylor, S.J.; Creasy, C.L.; Chernoff, J.; Cerione, R.A.  
J. Biol. Chem. 270, 22731-22737, 1995  
A>Title: Identification of a mouse p21Cdc42/Rac activated kinase.  
A/Reference number: I49376; MUID:96032693; PMID:7559398  
A/Accession: I49376  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: mRNA  
A/Residues: 1-544 <RES>  
A/Cross-references: UNIPROT:Q61036; EMBL:U09738; NID:G1079713; PIDN:AA652354.1; PID:G107  
A/Genetics:  
A:Gene: mPAK-3  
C/Superfamily: protein kinase homology  
C/Keywords: ATP  
F:266-519/Domain: protein kinase homology <KIN>  
F:274-282/Region: protein kinase ATP-binding motif

Query Match 29.4%; Score 907; DB 2; Length 544;

Best Local Similarity 34.6%; Pred. No. 1.1e-24; Matches 204; Conservative 90; Mismatches 169; Indels 126; Gaps 7;

Qy 4 KKKRVEISAPNFEHVRVTGPDHOKFTGLPRQMSLIE-----ESARRPKPLVLP 56  
Db 63 KKKEREISLPSDFHTIHVGPDVATVGEFTGPEQARLLQTSNITKLEQKKPQAVLD- 121  
Qy 57 ACTTISIQGAPRTIVGSGKADGALTLLDEFENMSVTRNSLRDSDPPPARAQENG 116  
Db 122 -----VLKFDSDKETVNNQKYSFT----- 141  
Qy 117 MPEBPTTARGGGKAGRGFRAGHSEAGGSGDRRRAGEPKKPSRSGSGGPOESSRD 176  
Db 142 -----SGDKSAGGYLAHQ-----SNTTKGSEPLAPVYSEEDDEEEDD 184  
Qy 177 KRPPLSGPDVGTPOPAAGLAKLAAGRPNTYPRADTDHPSRGAQGEPPHVAVPNGSAG 236  
Db 185 NRP---PVIARPRHTKS-----IYTRSVESIASPAANKEDIPPSAENMS 230  
Qy 237 LAIPOSSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPVPGPPGRSPQREP 296  
Db 231 TLTLYRTDR-----QRKK 243  
Qy 297 QRVSHQGFPAALQVJVDPPDPRSYLDFIKIGBSGTYCIATVRSSGKLVAKKMDLR 356  
Db 244 SKRTDEILIEKRSIVSVGDPKKRYTRLEKIGGASGAYTATADITGQVALKQNNLQQ 303  
Qy 357 QORRELLFNEVVMRDYOHENNVEMTNSYLVDGLVWMEFLEGALTDIVTTRNNEQ 416  
Db 304 QPKKEILIEILVMRENKPNIVYLDSTYVSGDELAVVMEYLAGSLTDVVTTCMDVQ 363  
Qy 417 IAAVCLAVIQLASVLAQGVIRHDIKSDSLTLTHDGRVKLSDFGCAQVSKVPRKSLV 476  
Db 364 IAAVCHRECLQALDPLHSNQVIHRDIKSDNILLQMDSSVKLTDFGCAQITPEQSKSTW 423  
Qy 477 GTPYMAPEVYTRKAGPVDIWSLGIIMAEWEGSPVLTNEMPAALVLIATNGPPEIQ 536  
Db 424 GTPYMAPEVYTRKAGPVDIWSLGIIMAEWEGSPVLTNEMPAALVLIATNGPPEIQ 483  
Qy 537 NHHKVSPLSKGLFDLLVDRPAQRATPAELIKHPFLAKAGPPASIVPLM 585  
Db 484 NPERLSAVPRDFLNRCLTENDVDRSGSAKELQHPPFLKAKPLSLPLI 532

## RESULT 5

protein kinase, p21-activated (EC 2.7.1.1) - human  
N:Alternate names: protein kinase PAK65; 56/H4 kinase  
C:Species: Homo sapiens (man)  
C>Date: 22-Aug-1996 #sequence\_revision 06-Sep-1996 #text\_change 16-Aug-2004  
C/Accession: S58682; S55258; S55304; S58690; A57441  
R:Sellis, M.; Knause, U.J.; Bagrodia, S.; Ambrose, D.; Bokoch, G.M.; Chernoff, J.  
submitted to the EMBL Data Library, April 1995  
A>Description: Human p21-activated protein kinases regulate actin organization in mammal  
A/Reference number: S58682

A/Accession: S58682  
A/Molecule type: DNA

A/Residues: 1-525 <SEL>

A/Cross-references: UNIPROT:Q13177; EMBL:U24153; NID:G780807; PIDN:AAA65442.1; PID:G7808  
R:Martin, G.A.; Bollag, G.; McCormick, F.; Abo, A.  
EMBO J. 14, 1970-1978, 1995

A>Title: A novel serine kinase activated by rac1/CDC42Ha-dependent autophosphorylation 1

A/Reference number: S55258; MUID:95262637; PMID:7744004

A/Accession: S55258

A>Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 'MEETQKSNEL', 31-89, 'T', 91-149, 'F', 151-224, 'T', 226-328, 'R', 330-338, 340-525

A/Accession: S55304

A/Molecule type: protein

A/Residues: 402-418 <MAW>  
R:Martin, G.A.; Bollag, G.; McCormick, F.; Abo, A.  
EMBO J. 14, 4385, 1995

A/Reference number: S58690; MUID:96016211; PMID:7556080

A/Accession: S58690

A>Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-30 <MAF>

R:Benner, G.E.; Dennis, P.B.; Maeracchia, R.A.  
J. Biol. Chem. 270, 21121-21128, 1995

A>Title: Activation of an 86/H4 kinase (PAK 65) from human placenta by intramolecular an

A/Reference number: A57441; MUID:95403344; PMID:7673144

A/Accession: A57441

A/Molecule type: protein

A/Residues: 197-216/402, 'S', 404-409 <BEN>

A/Experimental source: placenta

C/Superfamily: protein kinase homology

C/Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonin

F:247-501/Domain: protein kinase homology <KIN>

F:255-263/Region: protein kinase ATP-binding motif

F:197,402/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 29.0%; Score 895.5; DB 2; Length 525;

Best Local Similarity 34.9%; Pred. No. 2.7e-24; Matches 211; Conservative 94; Mismatches 136; Indels 163; Gaps 14;

Qy 4 KKKRVEISAPNFEHVRVTGPDHOKFTGLPRQMSLIE-----ESARRPKPLVLP 56  
Db 67 KKKEREISLPSDFHTIHVGPDVATVGEFTGPEQARLLQTSNITKLEQKKPQAVLD- 125  
Qy 57 ACTTISIQGAPRTIVGSGKADGALTLLDEFENMSVTRNSLRD--SPPPARAOE 114  
Db 126 -----VLKRYD-----SNTVQKQVLSFTPP-----EK 147  
Qy 115 NKMPE-EPATYTRAGGPGKAGRGFRAGHSEAGGSGDRRRAGEPKKPSRSGSGGPOES 173  
Db 148 DGLPSGTPLANKG-----TEA-----PAVTEEDDEDEBT 178  
Qy 174 SRDKRPLSGPDVGTPOPAAGLAKLAAGRPNTYPRADTDHPSRGAQGEPPHVAVPNGS 233  
Db 179 A-----PVIARPRHTKS-----IYTRSYTD-PVAPVDSH----- 210  
Qy 234 AGGLAIPOSSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPVPGPPGRSPQ 293  
Db 211 -----VDGAASLDRQ 221

```

OY 294 REBORSHOEPRALQVLVDPDPBPRSYLDFNFKIGEGSTGVICLATYRSSEKIYAAVKMD 353
Db 222 KKKPKMTDEIMKELKMTIVSIGPKKKYTRYKICQSGSVIFTRNDVALDQEVALKQIN 281
OY 354 LRKQORRELLFNEVIMRDYOHENNVEMYSYLVGDELMVMEFLBEGGALTDIVTHTR-M 412
Db 282 LOKOPKKELLINEILWKEKLNKNINIVNFDLSYLVGDELFVMEYIAGSGSLTDVVTETACM 341
OY 413 NEEQIAVCLAVIQAALSYVLAOCVIRHDIKSPISILLTDGKRYKSDPFCQAVQSEKVEYRR 472
Db 342 DEQIAIACVCECQIALEFLHANGVIHRDIKSNVLLMGESGYKLTDRFCQQITPEBSKR 401
OY 473 KSLVGTPLYMAAPELISRLPYGPEVDIWSIGIIVLEMVDSPEPPYENEPPLKAMKNIIDNLP 522
Db 402 STWVGTPYMAPEVYVIRKAYGPKVDIWSIGIIVLEMVDSPEPPYENEPPLKALYLIANTGT 461
OY 533 PRLKNIHKVSPSLKGFILRLVNDPAQORTAALELKHPLAKAGGPASIVL-----M 585
Db 462 PELONPKLSPIFRDPLNRCLEMDYKRSASAEILLQHFFLKIARPLSSLTTLIYMAAEAM 521
OY 586 RQNR 569
Db 522 KSNR 525

```

## RESULT 6

p21-activated protein kinase - human  
C|Species: Homo sapiens (man)  
C|Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 16-Aug-2004  
C|Accession: G01773  
R|Chernoff, J.  
submitted to the EMBL Data Library, April 1995  
A|Reference number: G08374  
A|Accession: G01773  
A|Status: preliminary; translated from GB/EMBL/DBJ  
A|Molecule type: mRNA  
A|Residues: 1-545 <CHE>  
A|Cross-references: UNIPROT:Q13153; EMBL:U24152; NID:g780805; PIDN:AAA65441.1; PID:g780808  
C|Genetics:  
A|Gene: Pak1  
C|Superfamily: protein kinase homology  
F|268-521|Domain: protein kinase homology <KIN>

[illegible]

QY	361	ELLFNEVIMROYCHENYEMWNSYLVADDELMVMEPEEGALDYITHIRNMBEOIAAV	420
	310	ELIINELIWMREKUNENINVIYDSTVADDELMVMEETIYAGSSLTVDVITBICMBEQOIAAV	369
Db	421	CLAVLOALSVLHAQGYIHRDIKSDSILTLTHDGKVKLSDFGCQAVSKVPRRSKSLVGPY	480
QY	370	CRECLOALBETHSNQYIHRDIKSDNIIILGOMGSVKLTDFGCQAITEGSKRSIMVGTPEY	429
Db	481	WMABELISRLPYGPEVWDIWSLGIWYIEKVDGPPYFENEPPLKAMKOTRDLNPLRLKYLK	540
QY	430	WMPEVUTRAKVGPKVDIWSLGIWYIEMIIEGEPPLINENPPLALYLLIATNGTPELOPEK	489
Db	541	VSSLSKGFDRLLNMPBARATAAALLHPPFLAKAGPASTVPLM	585
QY	490	LSAIFPDPFNRCCLMDMEKRSAGKALLDHQFLAKLAPLSSTPLI	534

## RESULT 7

S40482  
serine/threonine-specific protein kinase (EC 2.7.1.-) - rat  
C.Species: Rattus norvegicus (Norway rat)  
C.Date: 19-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-2004  
C.Accession: S40482  
R.Manser, E.; Leung, T.; Salihuddin, H.; Zhao, Z.; Lim, L.  
Nature 367, 40-46, 1994  
A.Title: A brain serine/threonine protein kinase activated by Cdc42 and Rac1.  
A.Reference number: S40482; PMID:94150588; PMID:8107774  
A.Accession: S40482  
A.Molecule type: mRNA  
A.Residues: 1-544 <MAN>  
C.Superfamily: protein kinase homology  
C.Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
F.267-520/Domain: protein kinase homology <KIN>  
F.275-283/Region: protein kinase ATP-binding motif

Query Match	28.9%	Score 892;	DB 2;	Length 544;
Best Local Similarity	36.9%	Pred. No. 3.6e-24;		
Matches 216; Conservative	82;	Mismatches 165;	Indels 122;	Gaps 11

[illegible]

Db 429 WMAPEVTRKAYGPKVDIWSLIGIMALEMIGEPPELYLENDRALYLITANGTELOQPEK 488  
QY 541 VPSLSLGLFDRLVRDPAORATAAEILKHPFLAKAGPASIPLM 585  
Db 489 LSAIFRDLNRCLEMDVEKRSKAKELLQHOFILAKPLSLTPLI 533

## RESULT 8

T18256  
probable serine/threonine-specific protein kinase (EC 2.7.1.-) - yeast (Candida albicans)  
C/Specties: Candida albicans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T18256  
R/Leberer, E.; Harcus, D.; Broadbent, I.D.; Clark, K.L.; Dignard, D.; Ziegelbauer, K.; S  
Proc. Natl. Acad. Sci. U.S.A. 93, 13217-13222, 1996  
A/Title: Signal transduction through homologs of the Ste20p and Ste7p protein kinases ca  
A/Reference number: Z18843; PMID:97075145; PMID:8917571  
A/Accession: T18256  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1230 <LEB>  
A/Cross-references: UNIPROT:O13431; EMBL:L47210; NID:g2276410; PID:g2286042; PIDN:AAB654  
C/Keywords: phosphotransferase; serine/threonine-specific protein kinase

Query Match 27.4%; Score 846.5; DB 2; Length 1230;  
Best Local Similarity 27.1%; Pred. No. 2.4e-22;  
Matches 221; Conservative 114; Mismatches 220; Indels 259; Gaps 17;

QY 1 MFGKRRK-----RVEISAPSNFEHRVHTGPDHOKFTGLPRWQSL 42  
Db 447 MFGKNKSTSSSSSSSGNSHSGQEVNIKISTFNAKHLAVGIDNN-GSYTGLPIEMERL 505  
QY 43 I-----ESARPRPLVDPACT--TSIQCAPRTIYVSGKAGDGLTLIDFENN 92  
Db 506 LSAIGITKKEQOHPQAVMDIVAFOYDTSNP-----DDAIFKFR--HFDNN 550  
QY 93 SVTRSNLSLRDSP-----PPARAENGMEPEEPATTARGC 128  
Db 551 KSSSSGMSMENTPPATPPGSSNGSGSGGAGAPSSPHRTPPSSIIENKNVQKITYTSQSM 610  
QY 129 PGKAGRGPRAGHSEAGGSGDRRRAGPEKRPKS--REGSGQPOESS--RDKRPLSGPDV 185  
Db 611 PRTTEK-----QSENHDPHEDNAQTGTPRTPTSHVQEQFIPSRAPAPKPSPTLSMSV 665  
QY 186 GTPQAPGLASGAKLAAGRPNTYPPRADTDHPSRGAQGEPHD----- 226  
Db 666 SHKTPSS-----QSLPRSDSQSDIRSTRPKSHQDVSPSKIKIRISISKSLKS 712  
QY 227 -----VAPNGPSAGLAIPQSSSSSRPPTRAGAPSPVLAGP----- 264  
Db 713 MRSKSGDKFTIAPAPPPPSLPSIPKSKSHSASLSQLRPATNGSTTAPIPASAAFGGE 772  
QY 265 -----HASEPQLAPACTPPAPAVPGPP----- 287  
Db 773 NNALPKQRIINEFAHAPAP--PPPSAPAPAPVPAPPAVNLSEGTSEIPQORTAPGALA 830  
QY 288 ----- 287  
Db 831 DVTAPNTIYEIQQTKYQEAQOKLREKARELEIORLREKNRQNRQOETGQNNADTASG 890  
QY 288 -----GPRSP-----OREPQVSHQEPRAALQOLVVDGDP 318  
Db 891 GSNIAFPVVPVPPKPPSGSGGGRDAKQALLAOKKREKGRKQLQIILAKLKITICNPDGP 950  
QY 319 SYLDNFIKIGEGSTGIVCIA--TVRSAGKLVAVKMDLRKQORRELLFNEVIMRDYOHEN 377  
Db 951 ELVVDLVKIGQAGSGGVFLAHVDVRKSNIVAIKQNMLEQPKKELLINELVWKSSHPN 1010  
QY 378 VEMNYSYLVGDELIVVMEFLBEGALTDITYTRAMEEQIAVCLAVLQALSTYLAQGY 437  
Db 1011 IYVFIISYLLKGLLWIMEMEBGSLDITYHVSMTGEOIGVCCRELLKGLKFLHSGVY 1070  
QY 438 HRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRRSKSLVCTPYMAAPELLSRIPYGPEDV 497

Db 1071 HRDIKSDNILLNMDGNIKITDFGCAQINEINSKRITTMGTPTVMAAPEIVSRKEGPKVD 1130  
QY 498 IMSLGIYVLEMDGEPPEYNEPPLKAMKIRNDLPRLKRLHVSLSLGLFDRLVLRP 557  
Db 1131 VMSLGIIMILEMGEPEPELYNETPLRALYLITANGTEPKLSDYDIRKFLAWCLQVDP 1190  
QY 558 AORATAEILKHPFLAKAGPASIPLMKNRTR 591  
Db 1191 NKRADDELHNDNFTECDVSSLSPLVKIARLK 1224

## RESULT 9

T18259  
serine/threonine protein kinase homolog - yeast (Candida albicans)  
C/Specties: Candida albicans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T18259  
R/Kohler, J.R.; Pink, G.R.  
Proc. Natl. Acad. Sci. U.S.A. 93, 13223-13228, 1996  
A/Title: Candida albicans straine heterozygous and homozygous for mutations in mitogen-  
A/Reference number: Z11118; PMID:97075146; PMID:8917572  
A/Accession: T18259  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1230 <KOH>  
A/Cross-references: UNIPROT:Q92212; EMBL:U73457; NID:g1657953; PID:g1737181; PIDN:AAB388  
C/Genetic:

Query Match 27.4%; Score 846.5; DB 2; Length 1230;  
Best Local Similarity 27.1%; Pred. No. 2.4e-22;  
Matches 221; Conservative 114; Mismatches 220; Indels 259; Gaps 17;

QY 1 MFGKRRK-----RVEISAPSNFEHRVHTGPDHOKFTGLPRWQSL 42  
Db 447 MFGKNKSTSSSSSSSGNSHSGQEVNIKISTFNAKHLAVGIDNN-GSYTGLPIEMERL 505  
QY 43 I-----ESARPRPLVDPACT--TSIQCAPRTIYVSGKAGDGLTLIDFENN 92  
Db 506 LSAIGITKKEQOHPQAVMDIVAFOYDTSNP-----DDAIFKFR--HFDNN 550  
QY 93 SVTRSNLSLRDSP-----PPARAENGMEPEEPATTARGC 128  
Db 551 KSSSSGMSMENTPPATPPGSSNGSGSGGAGAPSSPHRTPPSSIIENKNVQKITYTSQSM 610  
QY 129 PGKAGRGPRAGHSEAGGSGDRRRAGPEKRPKS--REGSGQPOESS--RDKRPLSGPDV 185  
Db 611 PRTTEK-----QSENHDPHEDNAQTGTPRTPTSHVQEQFIPSRAPAPKPSPTLSMSV 665  
QY 186 GTPQAPGLASGAKLAAGRPNTYPPRADTDHPSRGAQGEPHD----- 226  
Db 666 SHKTPSS-----QSLPRSDSQSDIRSTRPKSHQDVSPSKIKIRISISKSLKS 712  
QY 227 -----VAPNGPSAGLAIPQSSSSSRPPTRAGAPSPVLAGP----- 264  
Db 713 MRSKSGDKFTIAPAPPPPSLPSIPKSKSHSASLSQLRPATNGSTTAPIPASAAFGGE 772  
QY 265 -----HASEPQLAPACTPPAPAVPGPP----- 287  
Db 773 NNALPKQRIINEFAHAPAP--PPPSAPAPAPVPAPPAVNLSEGTSEIPQORTAPGALA 830  
QY 288 ----- 287  
Db 831 DVTAPNTIYEIQQTKYQEAQOKLREKARELEIORLREKNRQNRQOETGQNNADTASG 890  
QY 288 -----GPRSP-----OREPQVSHQEPRAALQOLVVDGDP 318  
Db 891 GSNIAFPVVPVPPKPPSGSGGGRDAKQALLAOKKREKGRKQLQIILAKLKITICNPDGP 950  
QY 319 SYLDNFIKIGEGSTGIVCIA--TVRSAGKLVAVKMDLRKQORRELLFNEVIMRDYOHEN 377  
Db 951 ELVVDLVKIGQAGSGGVFLAHVDVRKSNIVAIKQNMLEQPKKELLINELVWKSSHPN 1010

QY 378 VEMVNSYLVGDELAVWMEPELGGALTDIVTHTRMNEQIAVCLAVLQALSVLAAGVI 437  
DB 1011 IYNFIDSTYLGKDLWVIMWEGGSLTDIVHVSWTGQIGVCRFETLKGKFLHSGKVI 1070  
QY 438 HRDIKSDSILLTHDGRVSLDFGFCAYQSKVPRKSLVGTPTMMAPELISRLVYGEVD 497  
DB 1071 HRDIKSDSILLTMGNKILITDFGFCQJNEINSKRITVGTPTMMAPELISRKKEVGRVD 1130  
QY 498 IWSGIMVTEVNDGPPPTFNEPPLKAMKIRDLNLPRLKMLHKVSPSLKGFRLVLRDP 557  
DB 1131 VMSGIMVTEVNDGPPPTFNEPPLKAMKIRDLNLPRLKMLHKVSPSLKGFRLVLRDP 557  
QY 558 AQRATAELKGPFLAKGPPASIVPLMRQNR 591  
DB 1191 NKRADDELHNDFTTECDVSSLSPLVKARLK 1224

## RESULT 10

S28394  
probable serine/threonine-specific protein kinase (EC 2.7.1.1-) STE20 - yeast (Saccharomy  
N/Alternate names: protein YHL007C  
C/Species: Saccharomyces cerevisiae  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-2004  
R/Accession: S28394; S46821; A47324; A57493  
R/Rebeter, E.; Dignard, D.; Harcue, D.; Thomas, D.Y.; Whiteway, M.  
EMBO J. 11, 4815-4824, 1992  
A/Title: The protein kinase homologue Ste20p is required to link the yeast pheromone res  
A/Reference number: S28394; MUID:93099855; PMID:1464311  
A/Molecule type: DNA  
A/Residues: 1-939 <LEB>  
A/Cross-references: UNIPROT:Q03497; EMBL:M94719; NID:g172746; PIDN:AA35111.1; PID:g1727  
R/Faveilo, T.  
A/Description: The sequence of S. cerevisiae cosmid L5018.  
A/Reference number: S46798  
A/Accession: S46821  
A/Molecule type: DNA  
A/Residues: 1-939 <RAV>  
A/Cross-references: EMBL:U11581; NID:g508676; PIDN:AAB69747.1; PID:g508679; MIPS:YHL007C  
R/Pamer, S.W.; Davis, R.W.  
Proc. Natl. Acad. Sci. U.S.A. 90, 452-456, 1993  
A/Title: A dominant truncation allele identifies a gene, STE20, that encodes a putative  
A/Reference number: A47324; MUID:93133807; PMID:8421676  
A/Accession: A47324  
A/Molecule type: DNA  
A/Residues: 1-18, 'S', '20-133, 'M', '135-270, 'S', '272-939 <RAM>  
A/Cross-references: EMBL:L04655; NID:g172585; PIDN:AA35038.1; PID:g172586  
A/Note: sequence extracted from NCBI backbone (NCBI:122769, NCBI:122774)  
R/Wu, C.; Whiteway, M.; Thomas, D.Y.; Leberer, E.  
J. Biol. Chem. 270, 15984-15992, 1995  
A/Title: Molecular characterization of Ste20p, a potential mitogen-activated protein or  
A/Reference number: A57493; MUID:95332294; PMID:7608157  
A/Accession: A57493  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 757-784 <WTA>  
C/Genetics:  
A/Genes: SGD:STE20  
A/Cross-references: SGD:S0000999; MIPS:YHL007C  
A/Map position: 8L  
C/Function:  
A/Description: signal transduction; required for pheromone signal transduction  
C/Superfamily: protein kinase homology  
C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase; signal tr  
E/618-871/Domain: protein kinase homology <KIN>  
E/626-634/Region: protein kinase ATP-binding motif

Query Match 27 1%; Score 837; DB 2; Length 939;  
Best Local Similarity 32.3%; Pred. No. 4.1e-22;  
Matches 208; Conservative 98; Mismatches 191; Indels 146; Gaps 13;

QY 9 VEISAFNFEHRVHTGFDQEQFTGLPRQWOLIEESARRKPLVDPACITSIOPGAPK 68  
DB 335 LRISTPTYNKAIHHVGVDSKTEGYTLPEWKLITSGI 374  
QY 69 TIVRSGKAGDALTLILDEFE-NMSVTRNSLRDSDPPAPARQENGMEEPATARG 127  
DB 375 -----SKREQQNQMOAVMDIVAFYQDVTETNG-----EDKMFETFTT-G 414  
QY 128 GPQKAGSRFRPAHGEAGGSGDRRRAPBEKPKSREGSGGPPQSSSDKPELS 181  
DB 415 LFGS-----PQVST-----PPANSFNKPEPSTDSHN 441  
QY 182 -GPDVGTQPAAGLASGAKLAAGRPENTYPRADTHPSGAGPEHDVAPNPSAGLAIP 240  
DB 442 YSRRTGTPMSNIVMS-----PTLNTSSSANGFIRSPAPKPPSSASASAP 488  
QY 241 -----QSSSSSRPPTARCAPSPGVGPAS-----BPQLAPP----- 274  
DB 489 IIKSPVMSAAVNSPLKQTHAPPTPNRTSPNRSISRNALTKKEQPLPPIPTKSTSP 548  
QY 275 -----ACTPAPAVPGPPQPSQREPVSHS-----QFRALQ 309  
DB 549 IISTAHTEQVAAGSPKAPQSTVTTPTSKPAQASLSKELNEKREBERRRKQVAKLN 608  
QY 310 LVDPGDRSTYLDNFIKIGEGSTGICATVRSGLVAVKQDLRQQRRELFNEVVI 369  
DB 609 EICSDGDPSTYKAMLVKIGQAGSGVYTAIEIGTVSAIKOMVLKQPKKELIINILV 668  
QY 370 MRDVOHEVNVMSYLVGDELAVWMEPELGGALTDIVTHTRMNEQIAVCLAVLQALS 429  
DB 669 MKGSKRPVIVFIDSYLVKGDVWVIMWEGGSLTDIVHVSWTGQIGVCRFETLKGKFL 728  
QY 430 VLAQGVHNDIKSDSILLTHDGRVSLDFGFCAYQSKVPRKSLVGTPTMMAPELISR 489  
DB 729 FLHSGVLRDIKSDNILLMEGDIKLTDFGFCQJNEINLKTITVGTPTMMAPEVSR 788  
QY 490 LPYGEVDIVSLGIMVEMDGGPPPTFNEPPLKAMKIRDLNLPRLKMLHKVSPSLKGF 549  
DB 789 KEVGPKVDIVSLGIMVEMDGGPPPTFNEPPLKAMKIRDLNLPRLKMLHKVSPSLKGF 848  
QY 550 DRLVDRPAQRATAEELKGPFLAK-AGPPASIVPLMRQNR 591  
DB 849 DWICVPEPDRASATELLHDEYITTEIAENSSILAPLVKARLK 891

RESULT 11  
T39500  
serine/threonine-specific protein kinase (EC 2.7.1.1-) pak1-ehk1 - fission yeast (Schizos  
N/Alternate names: Ste20 homologous protein kinase 1  
C/Species: Schizosaccharomyces pombe  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 16-Aug-2004  
R/Accession: T39500; T45523  
R/Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, December 1998  
A/Reference number: Z21859  
A/Accession: T39500  
A/Molecule type: DNA  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Residues: 1-658 <BEC>  
A/Cross-references: UNIPROT:P50527; EMBL:AL034433; PIDN:CAA22347.1; GSPDB:GN00066; SPDB:  
A/Experimental source: strain 972h-, cosmid c1604  
R/Marcus, S.  
submitted to the EMBL Data Library, April 1997  
A/Reference number: Z22999  
A/Accession: T45523  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-658 <MAR>  
A/Cross-references: EMBL:L41552; PIDN:AAB52609.1  
C/Genetics:  
A/Genes: ehk1; SPBC1604.14C  
A/Map position: 1  
C/Superfamily: protein kinase homology

C/Keywords: hydrolase; phosphotransferase; signal transduction

Query Match 26.7%; Score 823.5; DB 2; Length 658;

Best Local Similarity 31.5%; Pred. No. 9e-22;

Matches 189; Conservative 113; Mismatches 193; Indels 103; Gaps 12;

QY 6 KKEVEISAPENFEHRYHTGFDQHEQKFTGLPRQMSLI-----ESARRPRLVDPAC 58

DB 142 RKSTVISPDPKHTVHGVNVDTEFTGMPTMQALTKVSGITKSGVOHPQAVLDAMA 201

QY 59 ITSIGAPAKTIVGSKAGKDGALTLILDFENMSVTRNSLRDSDPPARARQENGP 118

DB 202 FYS-----QSKYLEBGA-----KPPRESTEK----- 225

QY 119 EEPATTARGGPKAGSGRPFAGHSEAGSGGDRRRAGPEKPKSRSGSGGQPESSRDKR 178

DB 226 -----PLISVALSSSSHLQPTSATSSSRLYP-----SR 255

QY 179 PLSGPDVGTPOAGLASGAKLAAGRPNTPYPRADTHPSRGAQGEPHD--VAENGPAGG 236

DB 256 P-----APTPASSSSSPILSSQTVKTTNSARQPSPLVSSKSTDNIRSHSPV--- 305

QY 237 LAIPQSSSSSRPPTTARAGAPSPGVIGPFASEP--QLAPPACTPAPAPV---GPPGR 290

DB 306 LTPPTLTSETKHIR-----PNNSTPYQRAETSTKPKAVATQKVEAPSAAR 354

QY 291 SPQREQVSHQ--FRALQVLVDPDPRSYLDNFIKIGSGTGVCIATVRSGLVAV 349

DB 355 LQKRAAPQGSNDASVALAKQISICNPFTLLRNFKIQGASGDVYSARQVGTNLISVAL 414

QY 350 KKQDLRKQQRRELLFNEVIMEDYOHENVEMVNSYLVDGLVMVMEFLGALTDIVTH 409

DB 415 KKNINIQPKKEPIVNEILVMKSHHKINIVNIDTFEYKSELMMVMEYMGSLTEVTIN 474

QY 410 TRNNEQIAVCLAVIQALSVLHAQGVIRHDIKSDSILLTHGRVYKLSDFGCAQVSKY 469

DB 475 NTLSEQIAAIKCETELQHLHENGIVHRDIKSDNILLSLQGDIDLTDFGCAQIDSNM 534

QY 470 PRKSLVGTPTWMAPELISLTPYGEVDIWSIGIWIEMVDGPPFPNEPPLKAMKMRD 529

DB 535 TKRTTWGTPYMAPEVYTRKEYGFKVDVSLGIMAEVGEGBPYLNEPPLALYLIT 594

QY 530 NLPRLKMLHAKVPSLKGFLDRLVDRPAQRATAELLKHPFLAKGPPASIVPLMR 586

DB 595 IGTPIKSRPRLSSVHDFLSKSLTVNPKQRPSSGELLRHPLKQAVPSSILPLIK 651

## RESULT 12

S60170 protein kinase Pak1 - fission yeast (Schizosaccharomyces pombe)

C/Specter: Schizosaccharomyces pombe

C/Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 16-Aug-2004

C/Accession: S60170

R/Outfile: S.; Miller, P.J.; Johnson, D.I.; Creasy, C.L.; Sells, M.A.; Bagrodia, S.; For

EMBO J. 14, 5908-5919, 1995

A/Title: Fission yeast Pak1 (+) encodes a protein kinase that interacts with Cdc42p and 1

A/Reference number: S60170; MID:96112805; PMID:8846783

A/Accession: S60170

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-658 <OTT>

A/References: UNIPROT:P50527; EMBL:U22371; NID:g1122910; PIDN:AAC49125.1; PID:g112

C/Superfamily: protein kinase homology

C/Keywords: ATP

F/384-637/Domain: protein kinase homology <KIN>

F/392-400/Region: protein kinase ATP-binding motif

Query Match 26.4%; Score 814.5; DB 2; Length 658;

Best Local Similarity 31.3%; Pred. No. 1.8e-21;

Matches 187; Conservative 113; Mismatches 194; Indels 103; Gaps 12;

QY 6 KKEVEISAPENFEHRYHTGFDQHEQKFTGLPRQMSLI-----ESARRPRLVDPAC 58

DB 142 RKSTVISPDPKHTVHGVNVDTEFTGMPTMQALTKVSGITKSGVOHPQAVLDAMA 201

QY 59 ITSIGAPAKTIVGSKAGKDGALTLILDFENMSVTRNSLRDSDPPARARQENGP 118

DB 202 FYS-----QSKYLEBGA-----KPPRESTEK----- 225

QY 119 EEPATTARGGPKAGSGRPFAGHSEAGSGGDRRRAGPEKPKSRSGSGGQPESSRDKR 178

DB 226 -----PLISVALSSSSHLQPTSATSSSRLYP-----SR 255

QY 179 PLSGPDVGTPOAGLASGAKLAAGRPNTPYPRADTHPSRGAQGEPHD--VAENGPAGG 236

DB 256 P-----APTPASSSSSPILSSQTVKTTNSARQPSPLVSSKSTDNIRSHSPV--- 305

QY 237 LAIPQSSSSSRPPTTARAGAPSPGVIGPFASEP--QLAPPACTPAPAPV---GPPGR 290

DB 306 LTPPTLTSETKHIR-----PNNSTPYQRAETSTKPKAVATQKVEAPSAAR 354

QY 291 SPQREQVSHQ--FRALQVLVDPDPRSYLDNFIKIGSGTGVCIATVRSGLVAV 349

DB 355 LQKRAAPQGSNDASVALAKQISICNPFTLLRNFKIQGASGDVYSARQVGTNLISVAL 414

QY 350 KKQDLRKQQRRELLFNEVIMEDYOHENVEMVNSYLVDGLVMVMEFLGALTDIVTH 409

DB 415 KKNINIQPKKEPIVNEILVMKSHHKINIVNIDTFEYKSELMMVMEYMGSLTEVTIN 474

QY 410 TRNNEQIAVCLAVIQALSVLHAQGVIRHDIKSDSILLTHGRVYKLSDFGCAQVSKY 469

DB 475 NTLSEQIAAIKCETELQHLHENGIVHRDIKSDNILLSLQGDIDLTDFGCAQIDSNM 534

QY 470 PRKSLVGTPTWMAPELISLTPYGEVDIWSIGIWIEMVDGPPFPNEPPLKAMKMRD 529

DB 535 TKRTTWGTPYMAPEVYTRKEYGFKVDVSLGIMAEVGEGBPYLNEPPLALYLIT 594

QY 530 NLPRLKMLHAKVPSLKGFLDRLVDRPAQRATAELLKHPFLAKGPPASIVPLMR 586

DB 595 IGTPIKSRPRLSSVHDFLSKSLTVNPKQRPSSGELLRHPLKQAVPSSILPLIK 651

## RESULT 13

T15467 hypothetical protein C09B8.7 - Caenorhabditis elegans

C/Specter: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 16-Aug-2004

C/Accession: T15467

R/Stellies, L.

submitted to the EMBL Data Library, June 1995

A/Description: The sequence of C. elegans cosmid C09B8.

A/Reference number: S61138

A/Accession: T15467

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-622 <STE>

A/Cross-references: UNIPROT:Q17850; EMBL:U29612; NID:g868273; PID:g868279; PIDN:AAA6880

A/Experimental source: strain Bristol N2

C/Genetic:

A/Genes: C09B8.7

A/Intons: 107/1; 142/3; 192/1; 260/3; 291/3; 481/1; 505/3; 546/3; 570/3

C/Superfamily: protein kinase homology

Query Match 26.3%; Score 811.5; DB 2; Length 622;

Best Local Similarity 33.7%; Pred. No. 2.2e-21;

Matches 207; Conservative 87; Mismatches 175; Indels 145; Gaps 15;

QY 4 KKEKVE-----ISAPNFEHRYHTGFDQHEQKFTGLPRQMSLI-----ESARRPXP 52

DB 109 KDKKASEKRPVSRPSNFEHTIHVGVDPKTGFMPKAMARLTDQSISKQEQQNPQA 168

QY 53 LVDPACTITSIGAPAKTIVGSKAGKDGALTLILDFENMSVTRNSLRDSDPPARAR 112

DB 169 VLD-----ALKYTYQGSQGWLYQYMNDAPSRTPSYGLK----- 204

QY 113 QENGMPEEPATTARAGPKAGSGRPFAGHSEAGSGGDRRRAGPEKPKSRSGSGGQPE 172

Db 205 -----PQP 207  
Qy 173 SSRDRKPLSGPDVGTPOPAGLAGAKLAAGRPNITYPRADTDHPSRGAGSEPHDADNGP 232  
Db 208 YSTSSLPHYGNKNIQDRKKNKPMWTSISAG -YNS-----KQGVF-----P 246  
Qy 223 SAGGLAIPOSSSSSSPPPRARAGAPSPGVLPASER-QLAPACTPAAP----- 282  
Db 247 TTFVY---NENRSSNPSTY--App- --VPGETADIVPPA-IDRPATLSITTKP 295  
Qy 283 -----VP-----GPPPRS-PQRPQVSHQFRALQLVDPGDPSPSYLDFNFKIGEGS 331  
Db 296 KEEBEKIPDLKSGQPGVQARGQAKKKMTDAEVLTKLRITVISGNPDRKRVKVDKISGA 355  
Qy 332 TGIIVCIATVRRSSGSLVAVKMDLRKQORRELFREYVIMDYCHENVVENMNSTVNGEL 391  
Db 356 SGSVYTAIEISTAEFAVAKQMNLDQPKELINELIMENKRIANTVNYLDSYVDEL 415  
Qy 392 WYVMEELGEGALDITVHTMNEEQIAVACLAVALQALSVLAQGVIRHDIKSDSILLTHD 451  
Db 416 WYVMEELAGSGSLTDVVTTECOMEDGIIAAVCREVLQALEFLHSRAVIRHDIKSDNILLGMD 475  
Qy 452 GRVKLSDPFGCAQVSKEVPRKSLVGTPTVWMAPELISRLPYGPEVDYWSLGIMVTEYDG 511  
Db 476 GSVKLTDFGCAQLSPQRKRTTWGTPYMAPEVVRKQYGPXVDWVSLIMALEWEG 535  
Qy 512 EPPYFNEPPLKAMKMTKRDNLPRLLKNLHKVSPSLKGLFDRLLVDPQGRATVAELIKHPF 571  
Db 536 EPPYLNENPRLATYLLITNGKRPDPGRDSMTLLFKDFVDSLVEQVENKRWASQLTHPF 595  
Qy 572 LAKAGPPASIVPLM 585  
Db 596 LRCAKPLASLYLL 609

RESULT 14  
S60402  
N:Alternate names: protein K1A4 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)  
C:Species: Saccharomyces cerevisiae  
C:Date: 27-Apr-1996 #sequence revision 17-May-1996 #text\_change 16-Aug-2004  
C:Accession: S60402, S63274, S53103  
R:Maurer, K.C.T.; Urbanus, J.H.M.; Planta, R.J.  
Yeast 11, 1303-1310, 1995  
A:Title: Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV carrying a  
C. and a novel putative serine/threonine protein kinase gene.  
A:Reference number: S60394; MUID:96132033; PMID:8553702  
A:Accession: S60402  
A>Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-842 <MAN>  
A:Cross-references: UNIPROT:P48562; EMBL:U23084; NID:g1050853; PIDN:AAc49100.1; PID:g105  
submitted to the Protein Sequence Database, April 1996  
A:Reference number: S63266  
A:Accession: S63274  
A:Molecule type: DNA  
A:Residues: 1-842 <MAN>  
A:Cross-references: EMBL:271574; NID:g1302389; PIDN:CAa96216.1; PID:e239731; PID:g130238  
submitted to the Protein Sequence Database, April 1996  
R:Curkova, F.; Nasmyth, K.  
A:Description: STE20-like protein kinases are required for cytokinesis.  
A:Reference number: S53103  
A:Accession: S53103  
A:Molecule type: DNA  
A:Residues: 1-389, 'I', 391-842 <CVR>  
A:Cross-references: EMBL:h82499; NID:g732943; PIDN:CAa57879.1; PID:g732944  
A:Experimental source: strain K1107  
C:Genetics:  
A:Gene: SGD:CLA4; ERC10  
A:Cross-references: SGD:S0005242; MIPS:YNL298w

A:Map position:141L  
C:Superfamily: plectatrin repeat homology; protein kinase homology  
C:Keywords: ATP; phosphotransferase  
F:544-825/Domain: protein kinase homology <KIN>

Query Match 24.6%; Score 760; DB 2; Length 842;  
Best Local Similarity 31.2%; Pred. No. 1,6e-19;  
Matches 212; Conservative 99; Mismatches 239; Indels 130; Gaps 23;

QY 11 ISASNFEHRYHTGDFDHEOKFTGLRPWQSILIEESARRKPLVD--PACTSTIQ----- 63  
DB VSSPTNFTHKKVHFDEPTSGFVMPTMCKLKHSITIGEDMNNSAAVIQLQGYOEY 243  
QY 64 --PGAKTIYVGSAGADGALTLLDEFENSVTRNSI-----RDSRP 106  
DB NGAGNPNTTLDKPQSGETSSQSKSLPNSYNDNLKNNSVNSKSGSVSSMQRKTSQP 303  
QY 107 PPARARQENG-----MPEEPATTA---GGPKASRRPFAGSHSAGSGSDRRR 153  
DB PMTKSPVSLGSGSLPPINTKLPTSQSNIPHLQNVPRQQYPKPK-NCHSTTNG----QFP 358  
QY 154 AGPERKRPSRESGSGPDESRRDRP-----LSGPDVGTPOPAGLASAKLAAGRPFN 206  
DB RGMHPNNNSQSLQQQQQQQQQKHQYRYNHQCP---SPSPSPSPS-----PLN 407  
QY 207 TYPRADTDHPSRGAAGEPHDVAENGR---SAGGLAIPOSSSSSRPPTA-----RGAP 257  
DB 408 PY-----RPHHN-MINPYSKPOSPLSSOSTONQALPRYAQNSS--PTAHHPORPTAP 458  
QY 258 SGCVLGRIHASERQ-----LAP-----PACTPAFAVP---GPPGRRSPORE 295  
DB 459 KPIISAPRPAYPSNONATSNTHQPVAPKNDQSTPQMRAQPKRPDADVAPGGVAKPK 518  
QY 296 POR--VSHQEPPRALQLVVDPDPRSVDNFIKTGEGSTGVICIA-----TVRS----- 343  
DB 519 PARPMSTAEMISKVKATVANADBSQCFFVEKAQGAGSGSVYLAEKTHIPTESNMTELI 578  
QY 344 -----GKLVAVKNDLARKOQRRLTFEVVIMRDYOHENVEMYNSYL-VGDELNV 393  
DB 579 NNDIDEPHYGDVFAIKQWLVSQKPKEKLTIVELMKOSRKNINYNFLFAILRTDDDLNV 638  
QY 394 VNEFLLEGALTDIV-----TTRANNEBOIACVAVIALSYHAQGVIRHDIKSDS 445  
DB 639 VMEFMGGSLTIIINSPTPNDSHSLPTEPOLAVIVRETCCGLFKFIHDKHIHDIKSDN 698  
QY 446 ILITHDGRVKSDFGFCQAVSKVPRKSLVGTPPYMADELISLPVGEVDIMSGLMV 505  
DB 699 VLLDTAFARVKTIDFGCARLTDKRSKRAIMVTGTPYMADEVVAKQREIDEKIDVSLGIT 758  
QY 506 IENVVDSEPPYFMBPPLKAMKMIRDNLPRLLKNLHVYSLSLKGFLDRLLVDPDAQRATAE 565  
DB 759 IEMLBESPPLYLNEDPKALKLYLATNTGTPLKAGHRESLSLEIKRFSLVCVDVRYSATEE 818  
QY 566 LLMKPLAKAGPPASTIVPLM 585  
DB 819 LLHGHPFNMACDPKOLTSILL 838

RESULT 15  
T26684  
hypothetical protein y38f1A.10 - Caenorhabditis elegans  
C:Species:Caenorhabditis elegans  
C:Date:15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T26684  
R:Wallis, J.  
submitted to the EMBL Data Library, October 1998  
A:Reference number: Z20253  
A:Accession: T26684  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-378 <ML>  
A:Cross-references: UNIPROT:Q9XMTL8; EMBL:AL032639; PIDN:CAA21637.1; GSPDB:GN00020; CESP:  
A:Experimental source: Clone y38f1A





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 15, 2005, 10:58:31 ; Search time 199.897 Seconds

(without alignments)  
1513.973 Million cell updates/sec

Title: US-10-693-367-2

Perfect score: 3090  
Sequence: 1 MFGKKRKEVLSAPGNFEHR.....LAKAPPAIVPMQRNTR 591

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3090	100.0	591	1	PAK4_HUMAN
2	2860	92.6	593	1	PAK4_MOUSE
3	2856	92.4	597	2	Q6ZPX0
4	2853	92.3	593	2	Q80Z97
5	2558	82.8	501	2	Q8N4E1
6	2202.5	71.3	438	2	Q8NDE3
7	2202.5	71.3	467	2	Q8ULS8
8	2124.5	68.8	650	2	Q90M62
9	2031	65.7	663	2	Q6CM11
10	1967	63.7	407	2	Q8K0U2
11	1748	56.6	711	2	Q8C015
12	1745	56.5	711	2	Q6NVJ4
13	1740	56.3	719	2	Q8BV80
14	1731	56.0	719	1	PAK7_HUMAN
15	1730	56.0	719	2	Q8TB93
16	1501.5	48.6	639	1	PAK6_MOUSE
17	1501.5	47.7	681	1	PAK6_HUMAN
18	1473.5	47.4	558	2	Q7OGS5
19	1464.5	47.4	558	2	Q7OGS5
20	1241	40.2	240	2	Q8NCH5
21	1160	37.5	229	2	Q9CS71
22	1096.5	35.5	540	2	Q903M1
23	1090.5	35.3	542	2	Q18637
24	948.5	30.7	704	2	Q7OD76
25	937.5	30.3	704	2	Q24190
26	937.5	30.3	704	2	Q9V113
27	936	30.3	827	2	Q6IWN3
28	932.5	30.2	704	2	Q24213
29	924	29.9	544	1	PAK3_RAT
30	917	29.7	544	1	PAK3_RAT
31	907	29.4	577	2	Q803Z0

32	906.5	29.3	559	1	PAK3_MOUSE
33	905	29.3	577	2	Q6P017
34	904	29.3	524	1	PAK2_HUMAN
35	903	29.2	564	2	Q8AB4
36	900	29.1	524	1	PAK2_RABIT
37	895	29.0	524	1	PAK2_MOUSE
38	895	29.0	524	1	PAK2_RAT
39	894	28.9	524	2	Q6ISG3
40	894	28.9	544	1	PAK1_RAT
41	892.5	28.9	545	1	PAK1_HUMAN
42	891.5	28.9	559	1	PAK3_HUMAN
43	891.5	28.9	559	1	PAK3_PANTR
44	891.5	28.9	559	1	PAK3_PONPY
45	890	28.8	517	2	Q8AW67

## ALIGNMENTS

RESULT 1  
ID PAK4\_HUMAN STANDARD; PRT; 591 AA.  
AC Q96013; Q9BU33;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Serine/threonine-protein kinase PAK 4 (EC 2.7.1.37) (p21-activated kinase 4) (PAK-4).  
GN Name=PAK4;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=99043860; PubMed=9822598; DOI=10.1093/emboj/17.22.6527;  
RA Abo A., Ou J., Cammarano M.S., Dan C., Fritsch A., Baud V.,  
RA Bellefleur B., Minden A.,  
RT PAK4, a novel effector for Cdc42h, is implicated in the  
RT reorganization of the actin cytoskeleton and in the formation of  
RT filopodia.";  
RL EMBL J. 17:6527-6540(1998).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX Wehnich M.B.;  
RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strassberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettow K.H., Scheffer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heist F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Boser S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smaltz D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Activates the JNK pathway. Implicated in the  
CC reorganization of the actin cytoskeleton and in the formation of  
CC filopodia.



RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Matanabe Y., Wells C.,  
RA Waling L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hitozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shitaki T., Maki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RM [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVE/N, TISSUE=Colon;  
RX MEDLINE=22288557; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Umed T.B., Toshitoki S., Carninci P., Prange C.,  
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Boeck S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues R., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield J.S.N., Krzywicki M.T., Skalska U., Smalins D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- FUNCTION: Activates the JNK pathway. Implicated in the  
CC reorganization of the actin cytoskeleton and in the formation of  
CC filopodia (By similarity).  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- SUBUNIT: Interacts tightly with GTP-bound but not GDP-bound  
CC CDC42/p21 and weakly with RAC1 (By similarity).  
CC -1- PTM: Autophosphorylated when activated by CDC42/p21 (By  
CC similarity).  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. STE20  
CC subfamily.  
CC -1- SIMILARITY: Contains 1 CRIB domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
CC EMBL, AK088512; BAC40396.1; -;  
DR EMBL, BC048238; AAH48238.1; -;  
DR HSSP, Q13153; 1F3M.  
DR MGI:1917834; Pak4.  
DR InterPro: IPR011009; Kinase like.  
DR InterPro: IPR000095; Pakbox/Rhodning.  
DR InterPro: IPR000719; Ser\_Thr\_kinase.  
DR InterPro: IPR008271; Ser\_Thr\_pkin\_AS.  
DR InterPro: IPR002290; Ser\_Thr\_kinase.  
DR InterPro: IPR011026; Wasp\_C.  
DR Pfam: PF00786; PBD; 1.  
DR Pfam: PF00069; Kinase, 1.  
DR ProDom: PD000001; Prot\_Kinase, 1.  
DR SMART, SM00285; PBD; 1.  
DR SMART, SM00220; S\_TKC; 1.  
DR PROSITE, PSS0108; CRIB; 1.  
DR PROSITE, PSS0107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE, PSS0011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE, PSS0108; PROTEIN\_KINASE\_ST; FALSE NEG.  
KW ATP-binding; Phosphorylation; Serine/threonine-protein kinase;  
KW Transferase.  
FT DOMAIN 11 24 CRIB.  
FT DOMAIN 25 322 Linker.  
FT DOMAIN 323 574 Protein kinase.  
FT NP\_BIND 329 337 ATP (By similarity).  
FT BINDING 352 352 ATP (By similarity).  
FT ACT\_SITE 442 442 Protein acceptor (By similarity).  
SQ SEQUENCE 593 AA; 64622 MW; 4AFA91DD73D4C6D5 CRC64;  
Query Match 92.6%; Score 2860; DB 1; Length 593;  
Best Local Similarity 92.6%; Pred. No. 9.9e-98;  
Matches 550; Conservative 10; Mismatches 30; Indels 4; Gaps 2;  
QY 1 MEGKKRRVEISAPSNFEHVRVTGFDQHEQKFTGLPRQWOSLIESSARRPKLVDPACIT 60  
DB 1 MEGKKKKRVEISAPSNFEHVRVTGFDQHEQKFTGLPRQWOSLIESSARRPKLVDPACIT 60  
QY 61 SIQPGAPRTIVGSGKADGALTLLDDEFENNSVTRNSLRDSDPPPARAQENGMPE 120  
DB 61 SIQPGAPRTIVGSGKADGALTLLDDEFENNSVTRNSLRDSDPPPARAQENGMPE 120  
QY 121 PATTARGGPGKSGRPFAGHSEAGGSGDRRAGREKPKSREGSGGPOESSRDKPL 180  
DB 121 PATTARGGPGKSGRPFAGHSEAGGSGDRRAGREKPKSREGSGGPOESSRDKPL 180  
QY 122 RAAPAPMAPDKKSGRATGHSSEAGSGGDRRAGREKPKSREGSGGPOESSRDKPL 180  
DB 122 RAAPAPMAPDKKSGRATGHSSEAGSGGDRRAGREKPKSREGSGGPOESSRDKPL 180  
QY 181 SGPDVGTPOAGIASGAKLAAGRPNTVPRADTDHPSRGAQEPHDVAPNGSAGLAIP 240  
DB 181 SGPDVGTPOAGIASGAKLAAGRPNTVPRADTDHPSRGAQEPHDVAPNGSAGLAIP 240  
QY 182 SGPDVSTPGSLTSGTKLAAGRPNVTYPRADTDHPSRGAQEPHDVAPNGSAGLAIP 240  
DB 182 SGPDVSTPGSLTSGTKLAAGRPNVTYPRADTDHPSRGAQEPHDVAPNGSAGLAIP 240  
QY 241 QSSSSSSRPPTARAGPSGVTGPHASEPOLAPPA---CTPAAPAVPGGPGRSPPRREQ 297  
DB 241 QSSSSSSRPPTARAGPSGVTGPHASEPOLAPPA---CTPAAPAVPGGPGRSPPRREQ 297  
QY 242 QSSSSSSRPPTARAGPSGVTGPHASEPOLAPPA---CTPAAPAVPGGPGRSPPRREQ 299  
DB 242 QSSSSSSRPPTARAGPSGVTGPHASEPOLAPPA---CTPAAPAVPGGPGRSPPRREQ 299  
QY 298 RVSHQOPRALQLVDPGPPRSYLDNFKIGSGTIVCIATVRSRSGKVAKKMDLRQ 357  
DB 298 RVSHQOPRALQLVDPGPPRSYLDNFKIGSGTIVCIATVRSRSGKVAKKMDLRQ 357  
QY 300 RVSHQOPRALQLVDPGPPRSYLDNFKIGSGTIVCIATVRSRSGKVAKKMDLRQ 359  
DB 300 RVSHQOPRALQLVDPGPPRSYLDNFKIGSGTIVCIATVRSRSGKVAKKMDLRQ 359  
QY 358 QRRELLFNEVIMRDYOHENNVEMVNSYLVGDELVWMEFLGALTDIVTHRNMEQI 417  
DB 358 QRRELLFNEVIMRDYOHENNVEMVNSYLVGDELVWMEFLGALTDIVTHRNMEQI 417  
QY 360 QRRELLFNEVIMRDYOHENNVEMVNSYLVGDELVWMEFLGALTDIVTHRNMEQI 419  
DB 360 QRRELLFNEVIMRDYOHENNVEMVNSYLVGDELVWMEFLGALTDIVTHRNMEQI 419  
QY 418 AAVCLAVTALSVLAAGVTHRDYSDSLTHDGRVYKLSDFGCAQVSKVPRRSYLVG 477  
DB 418 AAVCLAVTALSVLAAGVTHRDYSDSLTHDGRVYKLSDFGCAQVSKVPRRSYLVG 477  
QY 420 AAVCLAVTALSVLAAGVTHRDYSDSLTHDGRVYKLSDFGCAQVSKVPRRSYLVG 479  
DB 420 AAVCLAVTALSVLAAGVTHRDYSDSLTHDGRVYKLSDFGCAQVSKVPRRSYLVG 479  
QY 478 TPYMAPELISRLPYGPEVDIWSLGIWTEWMDGPPYNEPPLKAMKIRDLNLPRLN 537  
DB 478 TPYMAPELISRLPYGPEVDIWSLGIWTEWMDGPPYNEPPLKAMKIRDLNLPRLN 537  
QY 480 TPYMAPELISRLPYGPEVDIWSLGIWTEWMDGPPYNEPPLKAMKIRDLNLPRLN 539  
DB 480 TPYMAPELISRLPYGPEVDIWSLGIWTEWMDGPPYNEPPLKAMKIRDLNLPRLN 539  
QY 538 LHKVPSLKGFLRLVNDPAQRATAEELKHPFLAKGPPASIVPLMKQNRTR 591  
DB 538 LHKVPSLKGFLRLVNDPAQRATAEELKHPFLAKGPPASIVPLMKQNRTR 591  
QY 540 LHKVPSLKGFLRLVNDPAQRATAEELKHPFLAKGPPASIVPLMKQNRTR 593  
DB 540 LHKVPSLKGFLRLVNDPAQRATAEELKHPFLAKGPPASIVPLMKQNRTR 593  
RESULT 3  
Q6ZPXO PRELIMINARY; PRT; 597 AA.  
ID Q6ZPXO;  
AC Q6ZPXO;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE MKIA1142 protein (Fragment).  
GN Name=mkIA1142;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryonic tail;

RX PubMed=14621295;  
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,  
 RA Suga Y., Nagase T., Ohara O., Koga H.;  
 RT "Prediction of the coding nucleotide sequences of 500 mouse KIAA gene:  
 RT I.I. the complete nucleotide sequences of 500 mouse KIAA-homologous  
 RT cDNAs identified by screening of terminal sequences of cDNA clones  
 RT randomly sampled from size-fractionated libraries.";  
 RL DNA Res. 10:167-180(2003).  
 DR EMBL: AK129298; BAC98108.1; -;  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO: GO:0004648; F:protein amino acid phosphorylation; IEA.  
 DR InterPro: IPR011009; Kinase like.  
 DR InterPro: IPR000095; PAKbox/Rho-binding.  
 DR InterPro: IPR000719; Prot\_kinase.  
 DR InterPro: IPR002290; Ser\_thr\_kinase.  
 DR InterPro: IPR011245; Tyr\_kinase.  
 DR InterPro: IPR011026; WASP\_C.  
 DR Pfam: PF00786; PBD; 1.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR ProDom: PD000001; Prot\_kinase; 1.  
 DR SMART: SM00285; PBD; 1.  
 DR SMART: SM00220; S\_TKC; 1.  
 DR SMART: SM00219; TyKc; 1.  
 DR PROSITE: PS50108; CRIB; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KM ATP-binding.  
 FT NON-TER  
 SQ SEQUENCE 597 AA; 64963 MW; 50C02613F77CCADA CRC64;

Query Match Best Local Similarity 92.4%; Score 2856; DB 2; Length 597;

Matches 549; Conservative 10; Mismatches 31; Indels 4; Gaps 2;

QY 1 MFGKKRKRVEISAPSNFHRVHTGPDQHEQKFTGLPRQWOSLIIESARRPKPLVDPACIT 60  
 DB 5 MFGKKRKRVEISAPSNFHRVHTGPDQHEQKFTGLPRQWOSLIIESARRPKPLVDPACIT 64  
 QY 61 SIQGPAPRTIYRSGKAGKADGALTLLDDEFENMSTRNSLRDSDPPPARAQENGMDEE 120  
 DB 65 SIQGPAPRTIYRSGKAGKADGALTLLDDEFENMSTRNSLRDSDPPPARAQENGMDEE 124  
 QY 121 PATTARGGPGKAGRGFRFAGSEAGSGGDRRAGPEKRPSSRSGSGPQESSRDRPL 180  
 DB 125 RVAPARMAPDKAGSARATGHSSEAGSGGDRRAGPEKRPSSRSGSGPQESSRDRPL 184  
 QY 181 SGPDVGTTPQAGLASGAKLAAGRPNNTYPRADTDHPSRGAQGEPRHDVAPNGPSAGLAIP 240  
 DB 185 SGPDVSTPQGSILTSGLTLAGRPNTYPRADTDHPRGAQGEPRHTMAPNGPSATGLAAP 244  
 QY 241 QSSSSSRPPTRRARAPSPVTLGPHASEPOLAPPA---CTPAAPAVGPPGPPRSPQREPO 297  
 DB 245 Q-SSSSSRPPTRRARAPSPVTLGPHASEPOLAPPA---CTPAAPAVGPPGPPRSPQREPO 303  
 QY 298 RVSHQGFRAALQVLVDPGDRSYLDNFIKIGSGTGVCIATVSSSGKLVAVKMDLRKQ 357  
 DB 304 RVSHQGFRAALQVLVDPGDRSYLDNFIKIGSGTGVCIATVSSSGKLVAVKMDLRKQ 363  
 QY 358 QRRRLLENEVIMRDYOHENYVEMNSYLVGDELMVNEFLEGALTDIVHTRNNEBOI 417  
 DB 364 QRRRLLENEVIMRDYOHENYVEMNSYLVGDELMVNEFLEGALTDIVHTRNNEBOI 423  
 QY 418 AAVCLAVIQLASVLAQGVTHRDIKSDSILLTHDGRVLSDFGCAQVSKVPRKSLVG 477  
 DB 424 AAVCLAVIQLASVLAQGVTHRDIKSDSILLTHDGRVLSDFGCAQVSKVPRKSLVG 483  
 QY 478 TPYMAAPRLISRLPGPEVDIMSLGIWTEWVGEPPYFNBPPLKAMMIRDNLPRLKN 537  
 DB 484 TPYMAAPRLISRLPGPEVDIMSLGIWTEWVGEPPYFNBPPLKAMMIRDNLPRLKN 543  
 QY 538 LHKVSPSLKGFLLDRLLVBDPAQRATPAELKHPLAKAGPPASIVPLMRQRTR 591

DB 544 LHKVSPSLKGFLLDRLLVBDPAQRATPAELKHPLAKAGPPASIVPLMRQRTR 597

RESULT 4  
 ID Q80297 PRELIMINARY; PRT; 593 AA.  
 AC Q80297;  
 DT 01-UTN-2003 (TrEMBLrel. 24, Created)  
 DT 01-UTN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE P21-activated protein kinase 4.  
 GN Name=PAK4;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=22526742; PubMed=12529371; DOI=10.1074/jbc.M205875200;  
 RA Lu Y., Pan Z.Z., Devaux Y., Ray P.;  
 RT "p21-activated protein kinase 4 (PAK4) interacts with the keratinocyte  
 RT growth factor receptor and participates in keratinocyte growth factor-  
 RT mediated inhibition of oxidant-induced cell death.";  
 RL J. Biol. Chem. 278:10374-10380(2003).  
 DR EMBL: AY217016; AAC61496.1; -;  
 DR HSBP; Q13153; 1F3W.  
 DR MGD; MGI:1917834; Pak4.  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO: GO:0004648; F:protein amino acid phosphorylation; IEA.  
 DR InterPro: IPR011009; Kinase like.  
 DR InterPro: IPR000095; PAKbox/Rho-binding.  
 DR InterPro: IPR000719; Prot\_kinase.  
 DR InterPro: IPR002290; Ser\_thr\_kinase.  
 DR InterPro: IPR011026; WASP\_C.  
 DR Pfam: PF00786; PBD; 1.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR ProDom: PD000001; Prot\_kinase; 1.  
 DR SMART: SM00285; PBD; 1.  
 DR SMART: SM00220; S\_TKC; 1.  
 DR PROSITE: PS50108; CRIB; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KM ATP-binding; Kinase.  
 SQ SEQUENCE 593 AA; 64666 MW; D7B3BD36706B4AF4 CRC64;

Query Match Best Local Similarity 92.3%; Score 2853; DB 2; Length 593;

Matches 550; Conservative 9; Mismatches 31; Indels 4; Gaps 2;

QY 1 MFGKKRKRVEISAPSNFHRVHTGPDQHEQKFTGLPRQWOSLIIESARRPKPLVDPACIT 60  
 DB 1 MFGKKRKRVEISAPSNFHRVHTGPDQHEQKFTGLPRQWOSLIIESARRPKPLVDPACIT 60  
 QY 61 SIQGPAPRTIYRSGKAGKADGALTLLDDEFENMSTRNSLRDSDPPPARAQENGMDEE 120  
 DB 61 SIQGPAPRTIYRSGKAGKADGALTLLDDEFENMSTRNSLRDSDPPPARAQENGMDEE 120  
 QY 121 PATTARGGPGKAGRGFRFAGSEAGSGGDRRAGPEKRPSSRSGSGPQESSRDRPL 180  
 DB 121 PATTARGGPGKAGRGFRFAGSEAGSGGDRRAGPEKRPSSRSGSGPQESSRDRPL 180  
 QY 181 SGPDVGTTPQAGLASGAKLAAGRPNNTYPRADTDHPSRGAQGEPRHDVAPNGPSAGLAIP 240  
 DB 181 SGPDVSTPQGSILTSGLTLAGRPNTYPRADTDHPRGAQGEPRHTMAPNGPSATGLAAP 240  
 QY 241 QSSSSSRPPTRRARAPSPVTLGPHASEPOLAPPA---CTPAAPAVGPPGPPRSPQREPO 297  
 DB 241 Q-SSSSSRPPTRRARAPSPVTLGPHASEPOLAPPA---CTPAAPAVGPPGPPRSPQREPO 299  
 QY 298 RVSHQGFRAALQVLVDPGDRSYLDNFIKIGSGTGVCIATVSSSGKLVAVKMDLRKQ 357

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Db 300 RVSHQFRAALQVDPGDSRLDIFIKIGESTGIVICATVRSSSGKLVAVKMDLRKQ 359
Qy 358 QRELLFNEVIMRDVGHENVENMNSYVGEDELVWMEFLREGALTDIVTRMNEBOI 417
Db 360 QRELLFNEVIMRDVGHENVENMNSYVGEDELVWMEFLREGALTDIVTRMNEBOI 419
Qy 418 AAVCLAVLQALSVLHAQGVYHDIKSDSILLTHDGRVKLSDFGCAQVSEKVEPRKSLVG 477
Db 420 AAVCLAVLQALSVLHAQGVYHDIKSDSILLTHDGRVKLSDFGCAQVSEKVEPRKSLVG 479
Qy 478 TTYMNAPELISRLPYGPEVDIWSLGIWVTEWVDGEPYPNEPPLKAMKIRDNLPRLKQ 537
Db 480 TTYMNAPELISRLPYGPEVDIWSLGIWVTEWVDGEPYPNEPPLKAMKIRDNLPRLKQ 539
Qy 538 LHKVPSLKGFLDRLVDPAPQATTAELIKHPFLAKAGPPASIVPLMKQNRTR 591
Db 540 LHKVPSLKGFLDRLVDPAPQATTAELIKHPFLAKAGPPASIVPLMKQNRTR 593

RESULT 5
Q8N4E1 PRELIMINARY; PRT; 501 AA.
AC Q8N4E1;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE PAK4 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE:2238257; PubMed:12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stalcenko M., Soares M.B., Bonaldo M.F., Casavant T.J., Scheetz T.E.,
RA Brownstein L.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loughlano N.A., Peters G.J., Abramson R.D., Millaby S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (Jul-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: BC034511, ANH34511.1; -
DR HSSP: Q13153, 1F3M.
DR GO: GO:0005524, F:ATP binding; IEA.
DR GO: GO:0004674, F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004648, F:protein amino acid phosphorylation; IEA.
DR InterPro: IPR011009; Kinase like.
DR InterPro: IPR000095; PAKbox/Rhodning.
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00786; PBD; 1.
DR Pfam: PF00069; Kinase; 1.

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DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PSS0108; CRIB; 1.
DR PROSITE; PSS0107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding.
SQ SEQUENCE 501 AA; 54940 MW; 6EE6240CE65E79D CRC64;

Query Match 82.8%; Score 2558; DB 2; Length 501;
Best Local Similarity 84.8%; Pred. No. 1e-86;
Matches 501; Conservative 0; Mismatches 0; Indels 90; Gaps 1;

Qy 1 MFGKRRKVEISAPSNFHRVHTGPDHQQKFTGLPRQWQSILIESARRPKPLVDPACTT 60
Db 1 MFGKRRKVEISAPSNFHRVHTGPDHQQKFTGLPRQWQSILIESARRPKPLVDPACTT 60
Qy 61 SIQGPAPKTIYVSGSKAKDGLTLLIDFENNSVTRSNLSRDSPPPPARAOENGMPEE 120
Db 61 SIQGPAPKTIYVSGSKAKDGLTLLIDFENNSVTRSNLSRDSPPPPARAOENGMPEE 120
Qy 121 PATTARGGPGKAGSGRPFAGHSEAGSGSDRRRAGEKPKSRBSGGPQSSRDKRL 180
Db 121 PATTARGGPGK-----GEPHVAANGPSAGGLAIP 150
Qy 181 SGPDVGTQPGAGLASGAKLAAGRFPNTYPRADTDHPSRGAGSEPHDVAENGPSAGGLAIP 240
Db 132 -----
Qy 241 QSSSSSSRPPTARAGAPSPGVLGPHASEPOLAPACTPAAPAVGPGGRRSPQREPORVS 300
Db 151 QSSSSSSRPPTARAGAPSPGVLGPHASEPOLAPACTPAAPAVGPGGRRSPQREPORVS 210
Qy 301 HQGFRAALQVDPGDSRLDIFIKIGESTGIVICATVRSSSGKLVAVKMDLRKQNR 360
Db 211 HQGFRAALQVDPGDSRLDIFIKIGESTGIVICATVRSSSGKLVAVKMDLRKQNR 270
Qy 361 ELLFNEVIMRDVGHENVENMNSYVGEDELVWMEFLREGALTDIVTRMNEBOIAYV 420
Db 271 ELLFNEVIMRDVGHENVENMNSYVGEDELVWMEFLREGALTDIVTRMNEBOIAYV 330
Qy 421 CLAVLQALSVLHAQGVYHDIKSDSILLTHDGRVKLSDFGCAQVSEKVEPRKSLVGT 480
Db 331 CLAVLQALSVLHAQGVYHDIKSDSILLTHDGRVKLSDFGCAQVSEKVEPRKSLVGT 390
Qy 481 WNAPELISRLPYGPEVDIWSLGIWVTEWVDGEPYPNEPPLKAMKIRDNLPRLKQNR 540
Db 391 WNAPELISRLPYGPEVDIWSLGIWVTEWVDGEPYPNEPPLKAMKIRDNLPRLKQNR 450
Qy 541 VSPSLKGFLDRLVDPAPQATTAELIKHPFLAKAGPPASIVPLMKQNRTR 591
Db 451 VSPSLKGFLDRLVDPAPQATTAELIKHPFLAKAGPPASIVPLMKQNRTR 501

RESULT 6
Q8NDE3 PRELIMINARY; PRT; 438 AA.
AC Q8NDE3;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hypothetical protein DKFZp547G182.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oanger A.,
RA Fobo G., Han M., Wiemann S.;

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RL Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: AL834236; CAD38914.2; -;  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO: GO:0004674; P:protein amino acid phosphorylation; IEA.  
 DR ATP-binding; Hypothetical protein.  
 SQ SEQUENCE 438 AA; 48267 MW; 4A596BECBCE9883 CRC64;

Query Match 71.3%; Score 2202.5; DB 2; Length 438;  
 Best Local Similarity 74.1%; Pred. No. 9.4e-74;  
 Matches 438; Conservative 0; Mismatches 0; Indels 153; Gaps 1;

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QY 1 MFGKKKKVEISAPNFEHRVHTGFDQHEQKFTGLPRQWQSLIESSARPKLVPACIT 60
DB 1 MFGKKKKVEISAPNFEHRVHTGFDQHEQKFTGLPRQWQSLIESSARPKLVPACIT 60
QY 61 SIQPGAPK----- 68
DB 61 SIQPGAPK----- 68
QY 121 PATTARGGGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGK 180
DB 69 ----- 68
QY 181 SGPDVGTQPPAGLAGAKLAAGRPNNTYPRADTHPSRGAQGEPRHDVAPNGPSAGLAIP 240
DB 69 ----- 87
QY 241 QSSSSSSRPPTARAGAPSPGVLGPHASEPOLAPACTPAAPAVPGPPGRSPQREPORVS 300
DB 88 QSSSSSSRPPTARAGAPSPGVLGPHASEPOLAPACTPAAPAVPGPPGRSPQREPORVS 147
QY 301 HEQFPAALQLVVDGDPSPSYLDFIKIGSGSTGIVCIATVRSSGKLVAVKMDLKKQQR 360
DB 148 HEQFPAALQLVVDGDPSPSYLDFIKIGSGSTGIVCIATVRSSGKLVAVKMDLKKQQR 207
QY 361 ELLFNEVIMRDYQHENVEMTNSYLVDGLVWMEFLGGLTIVTHTRNNEQIAAV 420
DB 208 ELLFNEVIMRDYQHENVEMTNSYLVDGLVWMEFLGGLTIVTHTRNNEQIAAV 267
QY 421 CLAVIALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPT 480
DB 268 CLAVIALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPT 327
QY 481 WMAPELLISRLPYGPEVDIWSIGIWIEMWDGEPFYFNEPPLKAMKIMRDNLPPRLKNLHK 540
DB 328 WMAPELLISRLPYGPEVDIWSIGIWIEMWDGEPFYFNEPPLKAMKIMRDNLPPRLKNLHK 387
QY 541 VSPSLKGFIDRLVDRDPQORATAELLKHPFLAKAGPPASIVPLMRQNRTR 591
DB 388 VSPSLKGFIDRLVDRDPQORATAELLKHPFLAKAGPPASIVPLMRQNRTR 438

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## RESULT 7

Q9ULS8 PRELIMINARY; PRT; 467 AA.

ID Q9ULS8  
 AC Q9ULS8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE KIAA1142 protein (Fragment).  
 GN Name=KIAA1142;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=20039618; PubMed=10574461;  
 RA Hirosawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;  
 RT "Characterization of cDNA clones selected by the Genemark analysis  
 from size-fractionated cDNA libraries from human brain.";

RL DNA Ref. 6:329-336(1999).  
 DR EMBL: AB032968; BAA86456.1; -;  
 DR HSRP; Q13153; 1F3M.  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO: GO:0004674; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR011009; Kinase like.  
 DR InterPro; IPR000095; PAKbox/Rho-binding.  
 DR InterPro; IPR000719; Prot. kinase.  
 DR InterPro; IPR002290; Ser/Thr\_pkinase.  
 DR InterPro; IPR011026; WASP\_C.  
 DR Pfam; PF00786; PBD; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Prodom; PD000001; Prot. kinase; 1.  
 DR SMART; SMO0285; PBD; 1.  
 DR SMART; SMO0220; S\_TKC; 1.  
 DR PROSITE; PS50108; CRIB; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW ATP-binding.  
 FT NON TER 1  
 SQ SEQUENCE 467 AA; 51464 MW; EC342B8F5C5B3940 CRC64;

Query Match 71.3%; Score 2202.5; DB 2; Length 467;  
 Best Local Similarity 74.1%; Pred. No. 9.9e-74;  
 Matches 438; Conservative 0; Mismatches 0; Indels 153; Gaps 1;

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QY 1 MFGKKKKVEISAPNFEHRVHTGFDQHEQKFTGLPRQWQSLIESSARPKLVPACIT 60
DB 30 MFGKKKKVEISAPNFEHRVHTGFDQHEQKFTGLPRQWQSLIESSARPKLVPACIT 89
QY 61 SIQPGAPK----- 97
DB 90 SIQPGAPK----- 97
QY 121 PATTARGGGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGK 180
DB 98 ----- 97
QY 181 SGPDVGTQPPAGLAGAKLAAGRPNNTYPRADTHPSRGAQGEPRHDVAPNGPSAGLAIP 240
DB 98 ----- 116
QY 241 QSSSSSSRPPTARAGAPSPGVLGPHASEPOLAPACTPAAPAVPGPPGRSPQREPORVS 300
DB 117 QSSSSSSRPPTARAGAPSPGVLGPHASEPOLAPACTPAAPAVPGPPGRSPQREPORVS 176
QY 301 HEQFPAALQLVVDGDPSPSYLDFIKIGSGSTGIVCIATVRSSGKLVAVKMDLKKQQR 360
DB 177 HEQFPAALQLVVDGDPSPSYLDFIKIGSGSTGIVCIATVRSSGKLVAVKMDLKKQQR 236
QY 361 ELLFNEVIMRDYQHENVEMTNSYLVDGLVWMEFLGGLTIVTHTRNNEQIAAV 420
DB 237 ELLFNEVIMRDYQHENVEMTNSYLVDGLVWMEFLGGLTIVTHTRNNEQIAAV 296
QY 421 CLAVIALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPT 480
DB 297 CLAVIALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPT 356
QY 481 WMAPELLISRLPYGPEVDIWSIGIWIEMWDGEPFYFNEPPLKAMKIMRDNLPPRLKNLHK 540
DB 357 WMAPELLISRLPYGPEVDIWSIGIWIEMWDGEPFYFNEPPLKAMKIMRDNLPPRLKNLHK 416
QY 541 VSPSLKGFIDRLVDRDPQORATAELLKHPFLAKAGPPASIVPLMRQNRTR 591
DB 417 VSPSLKGFIDRLVDRDPQORATAELLKHPFLAKAGPPASIVPLMRQNRTR 467

```

## RESULT 8

Q90W62 PRELIMINARY; PRT; 650 AA.

ID Q90W62  
 AC Q90W62;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)



DT 01-DEC-2001 (TEMBLrel. 19, last sequence update)  
 DT 01-OCT-2003 (TEMBLrel. 25, last annotation update)  
 DE PAKS protein.  
 GN Name=PAKS;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 NC NCBT\_TaxID=8355;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Stage VI oocyte;  
 RA Cau J., Faure S., Delaert C., Morin N.;  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ277826; CAC40979.1; -.  
 DR HSSP: Q13153; 1F3M.  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO: GO:0004668; F:protein amino acid phosphorylation; IEA.  
 DR Pfam: PF00786; PBD; 1.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR ProDom: PD000001; Prot\_kinase; 1.  
 DR SMART: SM00285; PBD; 1.  
 DR PROSITE: PS50108; CRIB; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW ATP binding.  
 SQ SEQUENCE 650 AA; 73736 MW; 9274DC6ACAD4A081 CRC64;  
 Query Match 68.8%; Score 2124.5; DB 2; Length 650;  
 Best Local Similarity 66.4%; Pred. No. 9.5e-71;  
 Matches 442; Conservative 43; Mismatches 90; Indels 91; Gaps 13;  
 QY 1 MFGRKRRVEISAPNFEHVRHTGPDHDEQKFTGLPROMOSTLIESARPKPLVDPACT 60  
 DB 1 MFGRKRRVEISAPNFEHVRHTGPDHDEQKFTGLPROMOSTLIESARPKPLVDPACT 60  
 QY 61 STPGAPKTIIVRSGKAKGALTLTLDPEFNSVTSNSLRDSP--PPPARQENG 117  
 DB 61 TTKHVPOKTIIVRSGKAKGALTLTLDPEFNSVTSNSLRDSP--PPPARQENG 117  
 QY 118 PE-----EPAITLRG----- 128  
 DB 118 PE-----EPAITLRG----- 128  
 QY 121 SEVRVQQRQEDGSGRSENRNREHRRERQREHRAVPOQPRGQEPNKKHPPPPDPKCI 180  
 DB 121 SEVRVQQRQEDGSGRSENRNREHRRERQREHRAVPOQPRGQEPNKKHPPPPDPKCI 180  
 QY 129 PGKAGSRGPFAGHSEAG-----GSGD-----RRAGPEKPKS-REGSGAPQ 172  
 DB 129 PGKAGSRGPFAGHSEAG-----GSGD-----RRAGPEKPKS-REGSGAPQ 172  
 QY 181 PEKRGPR-----SHEKSGRREYVGNDRGHSDPYERVVKKDKGEKKPKSAVTSGEGSPQ 235  
 DB 181 PEKRGPR-----SHEKSGRREYVGNDRGHSDPYERVVKKDKGEKKPKSAVTSGEGSPQ 235  
 QY 173 SSRDRKPLSGPDVGTPOAGLASGAY-LAAGRPNTYPRADTDHPSRGAQGEPRDVA 231  
 DB 173 SSRDRKPLSGPDVGTPOAGLASGAY-LAAGRPNTYPRADTDHPSRGAQGEPRDVA 231  
 QY 236 SPRDRKPLSGPNRTGSSSTGSDGVVQGTGRFPNTYPRAEPTD-PRGAAHQVSDSRSTV 294  
 DB 236 SPRDRKPLSGPNRTGSSSTGSDGVVQGTGRFPNTYPRAEPTD-PRGAAHQVSDSRSTV 294  
 QY 232 P-----SAGGLAIPSSSSSSSPRRARAGAPRGVLGPHASPOLAPACTPAARAVNG 285  
 DB 232 P-----SAGGLAIPSSSSSSSPRRARAGAPRGVLGPHASPOLAPACTPAARAVNG 285  
 QY 295 PLDSKSSVSRSRPPQGGVKKPPEK---PPTQLAPHSPOLSRPQT-----QH 344  
 DB 295 PLDSKSSVSRSRPPQGGVKKPPEK---PPTQLAPHSPOLSRPQT-----QH 344  
 QY 286 PPGPRSPQREPOVSHQEPFAALQLVDDPDPSYLDNFITKIGEGTGIVCIATVSSGK 345  
 DB 286 PPGPRSPQREPOVSHQEPFAALQLVDDPDPSYLDNFITKIGEGTGIVCIATVSSGK 345  
 QY 345 PQGRSPQREPOVSHQEPFAALQLVDDPDPSYLDNFITKIGEGTGIVCIATVSSGK 404  
 DB 345 PQGRSPQREPOVSHQEPFAALQLVDDPDPSYLDNFITKIGEGTGIVCIATVSSGK 404  
 QY 346 LVAVKKMDLRKQGRRELLFNEVVIMRDYQEHNVEMVNSYLVGDELAVNMEFLGALTD 405  
 DB 346 LVAVKKMDLRKQGRRELLFNEVVIMRDYQEHNVEMVNSYLVGDELAVNMEFLGALTD 405  
 QY 405 LVAVKKMDLRKQGRRELLFNEVVIMRDYQEHNVEMVNSYLVGDELAVNMEFLGALTD 464  
 DB 405 LVAVKKMDLRKQGRRELLFNEVVIMRDYQEHNVEMVNSYLVGDELAVNMEFLGALTD 464  
 QY 406 IYHTHMEHQIATVCLAVYALSVYHAQGVTHRDIKSSIIITLTHGRVYLSFGCAQV 465  
 DB 406 IYHTHMEHQIATVCLAVYALSVYHAQGVTHRDIKSSIIITLTHGRVYLSFGCAQV 465  
 QY 465 IYHTHMEHQIATVCLAVYALSVYHAQGVTHRDIKSSIIITLTHGRVYLSFGCAQV 524  
 DB 465 IYHTHMEHQIATVCLAVYALSVYHAQGVTHRDIKSSIIITLTHGRVYLSFGCAQV 524  
 QY 466 SKEVPRKSLVGTPTVMAPELLIRLPYGPVNDIWSIGIMVEMVNDGPPYFNEPPLKAK 525  
 DB 466 SKEVPRKSLVGTPTVMAPELLIRLPYGPVNDIWSIGIMVEMVNDGPPYFNEPPLKAK 525  
 QY 525 NKEVPRKSLVGTPTVMAPELLIRLPYGPVNDIWSIGIMVEMVNDGPPYFNEPPLKAK 564  
 DB 525 NKEVPRKSLVGTPTVMAPELLIRLPYGPVNDIWSIGIMVEMVNDGPPYFNEPPLKAK 564

QY 526 MTRDNLPRLLKNIHKVSPSLKGLDRLTYRDPAPORATABLKHPPIAKAGPPASTVPLM 585  
 DB 585 MTRDNLPRLLKNIHKVSPSLKGLDRLTYRDPAPORATABLKHPPIAKAGPPASTVPLM 644  
 QY 586 RQNRTR 591  
 DB 645 RQNRTR 650  
 RESULT 9  
 ID 06GM11 PRELIMINARY; PRT; 663 AA.  
 AC 06GM11;  
 DT 05-JUL-2004 (TEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)  
 DE Zgc:92014.  
 GN ORFNames=zgc:92014;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NC NCBT\_TaxID=7955;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaller G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Caasvant T.L., Schetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Hellon E., Kettleman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Matra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC074067; AAH74067.1; -.  
 DR ZFIN: ZDB-GENE-040704-69; zgc:92014.  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO: GO:0004668; F:protein tyrosine kinase activity; IEA.  
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR InterPro: IPR011026; Kinase like.  
 DR InterPro: IPR000095; PAKbox/Rhodning.  
 DR InterPro: IPR000719; Prot\_kinase.  
 DR InterPro: IPR002290; Ser\_thr\_kinase.  
 DR InterPro: IPR001245; Tyr\_kinase.  
 DR InterPro: IPR011026; WAPC\_C.  
 DR Pfam: PF00786; PBD; 1.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR ProDom: PD000001; Prot\_kinase; 1.  
 DR SMART: SM00285; PBD; 1.  
 DR SMART: SM00220; S\_TKc; 1.  
 DR SMART: SM00219; TyKc; 1.  
 DR PROSITE: PS50108; CRIB; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.

DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KR	ATP-binding. 663 AA; 74760 MW; 616BF69876E40550 CRC64;
SO	SEQUENCE
Query Match	65.7%; Score 2011; DB 2; Length 663;
Best Local Similarity	62.0%; Pred. No. 2,6e-67;
Matches 427; Conservative 50; Mismatches 89; Indels 124; Gaps 16	
QY	1 MFGKKK-RVELSAASNFHRVHTGPDQHEQKFTGLPRQWQSLIESARPRPLNDPACT 59
DB	1 MFSKKKKRIQISAASNFHRVHTGPDQHEQKFTGLPRQWQSLIESARPRPLNDPACT 60
QY	60 TSIQGAPEPTVYRSGKAGKADGALLTLDDFENMSYTRNSLRDSSP----- 106
DB	61 TTVEE--KRTIVRGKIKGDDGSLTWLDDFETMSYTRNSLSLRGSPPLQPRDSSGSGGH 118
QY	107 -----PPARAQENGMPEEPTATYAG-- 127
DB	119 ENGHEPQYRHTDTRVYDSKERERKPEQENPPTDQSGRPFGRSSRDGRPQQ--QPRGQAP 175
QY	128 -----GPGKASRGR-----FAGHEAAGCGSDRRRAGERPKSRBSSGGP 170
DB	176 SRHKRPDWTTPQCHREKEREKREPRDYSDHV-----KREGANDKPKSYTGRDSS 228
QY	171 QESSRDKRPLSGPDVGTDP--PAGIASGAKLAAGRPFNTYPRADT-----HPS 217
DB	229 PQSPREKRPPLSGPFIPTPLPTVEGVIKAQ-QGTGRFNTYPRSSDSGRTPSGQDLKPA 287
QY	218 RGAQGEPRHDVAANGSAGGALIPSSSSSSRRPPTARAKAPSGVGLCPHASEFQ--LAPPA 275
DB	288 KSHESTNH---NGESAG--PVRGSSSSS-----GGQTSQGPHRSEPHASHPA 334
QY	276 CTPAAP---AVGPPPGP-----RSPQREPORVSHQERFALQLVVDGDPSTYD 322
DB	335 LGPEPRHQPMPPRPKPSGAPASQQTSSPQREPRQVSHQERFALQLVVDGDPSTYD 394
QY	323 NFIRKIGEGSTGICATVTRSSGKLVAVKMDLRKQORRELLFNEVYIMRDYQHENVEMY 382
DB	395 HYIKIGEGSTGICATVTRTKGLVAVKMDLRKQORRELLFNEVYIMRDYHNEVEMY 454
QY	383 NSYLVDDELVMVMEFLREGALTDIYTHPTMNEEQIATAVCLALQALSVLAAGVTHRDIK 442
DB	455 NSYLVDDELVMVMEFLREGALTDIYTHPTMNEEQISTVCLSVKALSVLHSGVTHRDIK 514
QY	443 SDSILLTHDGRVKSDFGFCAGVSKVEPRRSKSLVGTPIYMADELISRLPYGGEVDIWSLG 502
DB	515 SDSILLTHDGRVKSDFGFCAGVSKVEPRRSKSLVGTPIYMADELISRLPYGGEVDIWSFG 574
QY	503 IMVIEVMDGEPPEYFNEBPLKAMKMTKRDNPRLTKNLIHKVPSLKGTLDTLVRDPAQRAT 562
DB	575 IMVIEVMDGEPPEYFNEBPLKAMKMTKRDNPRLTKNLIHKVPSLKGTLDTLVRDPAQRAT 634
QY	563 AAEILKHPEFLAKAGPPASIVPLMRQNRTR 591
DB	635 AQEILKHPEFLTKAGPPSCIVPLMRQNRK 663
RESULT 10	
Q8K0U2	PRELIMINARY; PRT; 407 AA.
AC	Q8K0U2;
DT	01-OCT-2002 (Tremblrel. 22, Created)
DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE	Pak4 protein (Fragment).
GN	Name=Pak4;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_Taxid=10090;
KN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Eye;

[illegible]

Db 366 DRLLVRDPAQRATAELLKHPFLTAKGPPASIVPLMRQHRT 407

[illegible]



OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Mech. Enzymol. 303:19-44(1999).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;  
 RX The FANTOM Consortium;  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;  
 RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;  
 RX MEDLINE=20550913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 Kono H., Akiyama J., Nishi K., Kiteunai T., Taenirio H., Itoh M.,  
 Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
 Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,  
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,  
 Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;  
 RX Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,  
 Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 Hayashida K., Hayatsu N., Hiramoto K., Hiramoto T., Hirozane T.,  
 Hori F., Imetani K., Ishii Y., Itoh M., Kikawa I., Kasukawa T.,  
 Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,  
 Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 Nishi K., Nomura K., Numazaki R., Ono M., Ohnato N., Okazaki Y.,  
 Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,  
 Tagawa A., Takahashi F., Takeki-Akashira S., Takeda Y., Tanaka T.,  
 Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL AK079080; BAC37528.1; -.  
 DR HSSP; Q3153; 1F3M.  
 DR MGD; MG1:1920334; Pak7.  
 DR GO; GO:0005739; C:mitochondrion; IDA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.  
 DR GO; GO:0006166; P:anti-apoptosis; IDA.  
 DR InterPro; IPR011009; Kinase\_Like.  
 DR InterPro; IPR000095; PAKbox/Rhodning.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR011026; WSP\_C.

DR Pfam; PF00786; PBD; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00285; PBD; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS50108; CRIB; 1.  
 DR PROSITE; PS50109; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR ATP-binding; Kinase.  
 DR SEQUENCE 719 AA; 80967 MW; F1E33DCB8C39875B CRC64;  
 QY Query Match 56.3%; Score 1740; DB 2; Length 719;  
 Best local Similarity 52.7%; Pred. No. 1,3e-56;  
 Matches 384; Conservative 65; Mismatches 129; Indels 150; Gaps 16;  
 1 MFGRKRKRVEISAPNSFEHRVHTGPDQHQKFTGLPRQMSLIESARRPKPLVDPACIT 60  
 1 MFGRKKKKKLEISGPSNFEHRVHTGPDQHQKFTGLPRQMSLILADTANRPKPMDPSCIT 60  
 61 STPGAPKTIIVGSKAKDGLTLLEDFENMSVTRSNLRDSDPP--RAR----- 112  
 61 PQLAPMKTIIVGNKSKETSINGLLEDDNLSVTRSNLRKSPPTPDGAASRIQGS 120  
 113 QENGM-----PEEPATTARGGPGKASRGRA-----GH----- 141  
 121 EENGFITFSQYSESDTTADYTTETKRDLSLYGDDLDLYKSHAKONGHAMKMGDA 180  
 142 -----SEAGSGSGDRRA----- 154  
 181 YYPEMKSILKTDLAPVDYHTLDSLRKSEYGLRWYQYRASSGSLDYSFQLTPSPRTA 240  
 155 -----GR-----EKRPKSNREGSGPPESSRDRLPSGPVGT--QRA 191  
 241 GTSRCKESLAVSESDWGPSLDYDRPKRSYLAQTSPPQAMR-QKSKSGSGIQEPMMP 299  
 192 GLASGAKLAAGRPNTY-----PRADTDH-----PSRGAQGEPHDVANGP 232  
 300 GASAPFTHQGSYSNTYTPRLSEPTMCTPKDYDRAQVWPSPPLSGS-----DYTPRP 354  
 233 SAAGLAIPQS-----SSSSSRPPTRARGA-----PSPGVLAGHASEPQLAPACTPAAP 281  
 355 T-----KLPGSQSKAGYSSGSHQYPSGYNHAKSLYHHPSLQTSQYISTAGYL--SSLISSS 409  
 282 AVPGPGRPSPPREPRQVNEHQFRALQLVDPGPRSLTDMFIKIGESTGIVCAATVR 341  
 410 TYPPEWSSSSQOQPSRVSHEQFRALQLVSPGPRELQDNFIKIGESTGIVCAATEK 469  
 342 SSGKLVAVKMDLRKQQRRELLFNEVVIIMRDYQEHNVEMVNSYLVGDELMVMEFLREG 401  
 470 HTGQVAVAKMDLRKQQRRELLFNEVVIIMRDYHHDVNDVMSYLVGDELMVMEFLREG 529  
 402 ALTDIVTTRNMEBOIAVCAVLQALSVLAQGVIRDKSDSILLTHDGRVKLSDFGR 461  
 530 ALTDIVTTRNMEBOIAVCAVCLSVLAKLSVLAHQGVIRDKSDSILLTSDGRVKLSDFGR 589  
 462 CAQVSKVPRKSLVGTPTWMAPELISRLPYGPBVNDISLGMVEMVNDGEPYFPEPL 521  
 590 CAQVSKVPRKSLVGTPTWMAPEVLSRLPYGTEVDIWSLGMVEMVNDGEPYFPEPL 649  
 522 KMKMIRNDLPRLKVLHVSPSLKGFDRLLVDPDAQATAAELLKHPFLAKGAPASI 581  
 650 QAMRRIRDSLPVRKDLHVKVSMLKGFDDMLVREPSQATAOELLGHFFLKLADGPSCT 709  
 QY 582 VPLMRQNR 589  
 DB 710 VPLMRQYR 717  
 RESULT 14  
 ID PAK7 HUMAN STANDARD; PRT; 719 AA.  
 AC Q9P286; Q9P286; Q9P286; Q9P286;  
 DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCR-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel.44, Last annotation update)  
 DE Serine/threonine-protein kinase PAK 7 (EC 2.7.1.37) (p21-activated  
 DE kinase 7) (PAK-7) (PAK-5).  
 GN Name=PAK7; Synonyms=XKIA1264, PAK5;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22020812; PubMed=12032833; DOI=10.1038/sj/om/1205478;  
 RA Pandey A., Dan I., Krieriansen T.Z., Watanabe N.M., Volody J.,  
 RA Kajikawa E., Khosravi-Par R., Bligoev B., Mann M.,  
 RT "Cloning and characterization of PAK5, a novel member of mammalian  
 RT p21-activated kinase-II subfamily that is predominantly expressed in  
 RT brain".  
 RL Oncogene 21:3939-3948 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=20039619; PubMed=10574462;  
 RA Nagase T., Ishikawa K.-I., Kikuno R., Hiroseawa M., Nomura N.,  
 RA Ohara O.,  
 RT "Prediction of the coding sequences of unidentified human genes. XV.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins in vitro".  
 RL DNA Res. 6:337-345 (1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;  
 RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,  
 RA Jones M., Steviers G., Almeida J.P., Babbsge A.K., Baguley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Chapman D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Cundy N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dohy M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Leharaslatio M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McCormack L.J., McClay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.P., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prithalingam S.R., Plumb R.W., Ramsey H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sella H.K., Showkhen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Suleston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A.C., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Whitting L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.,  
 RT "The DNA sequence and comparative analysis of human chromosome 20".  
 RL Nature 414:865-871 (2001).  
 CC -1- FUNCTION: The activated kinase acts on a variety of targets (By  
 CC similarity).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- SUBUNIT: Interacts tightly with GTP-bound but not GDP-bound  
 CC CDG42/p21 and Rac1 (By similarity).  
 CC -1- TISSUE SPECIFICITY: Predominantly expressed in brain.  
 CC -1- PTM: Autophosphorylated when activated by CDG42/p21 (By  
 CC similarity).  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. STE20  
 CC subfamily.  
 CC -1- SIMILARITY: Contains 1 CRIB domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration -  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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	CC	or send an email to <a href="mailto:license@ebi.ac.uk">license@ebi.ac.uk</a> .
	CC	-----
	DR	EMBL; AB040812; BAA94194.1; -
	DR	EMBL; AB033090; BAA6578.1; ALT_INIT.
	DR	EMBL; AL353612; CAC34367.1; -
	DR	HSSP; Q13153; IFSM.
	DR	H-geneDB; HIX0015637; -
	DR	MIM; 608038; -
	DR	InterPro; IPRO11009; Kinase like.
	DR	InterPro; IPRO00095; PAKbox/RhoGing.
	DR	InterPro; IPRO00719; Prot. kinase.
	DR	InterPro; IPRO08271; Ser thr_pkin_AS.
	DR	InterPro; IPRO02290; Ser thr_kinase.
	DR	InterPro; IPRO1026; WASP_C.
	DR	Pfam; PF00786; PBD; 1.
	DR	Pfam; PF00069; Kinase; 1.
	DR	ProDom; PD000001; Prot_kinase; 1.
	DR	SMART; SM00285; PBD; 1.
	DR	SMART; SM00220; STKc; 1.
	DR	PROSITE; PS50108; CRIB; 1.
	DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.
	DR	PROSITE; PS50011; PROTEIN KINASE DOM; 1.
	DR	PROSITE; PS00108; PROTEIN KINASE ST; FALSE NEG.
	KW	ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
	KW	transrase.
	FT	DOMAIN 11 24 CRIB.
	FT	DOMAIN 25 448 Linker.
	FT	DOMAIN 449 700 Protein kinase.
	FT	NP BIND 455 463 ATP (By similarity).
	FT	BINDING 478 478 ATP (By similarity).
	FT	ACT SITE 568 568 Proton acceptor (By similarity).
	SQ	SEQUENCE 719 AA; 80744 MW; 07A12B1EC4E2A02 CRC64;
	Query Match	56.0%; Score 1731; DB 1; Length 719;
	Best Local Similarity	52.4%; Pred. No. 2.7e-56;
	Matches 383; Conservative	66; Mismatches 126; Indels 156; Gaps 17;
OY	1	MEGRKKRVEISASNPENRHYNTHPEPDCHOKEFGLPRQMOSLIESARPKPLVDPACT 60
DB	1	MFGRKKRIETIGSGSNFEHRVHTGDPOEQFTGLPQQMHSLLDAPRKPMWDPSCTT 60
OY	61	SIQCAPRTIYRGSKGAKDGALTTLLDEFENMSYTRNSLRDSPPPARA-----R 112
DB	61	PIQLAPMTIYRGKMKCKETSINGLEDFODISYTRSLSLKESPTPDGASSHPGHA 120
OY	113	QENGK-----PEEPATTA-----RG--PKA 132
DB	121	EENGETTFPSQYSSSDTDADYTTEREKSLDYGDLDLYRGSNAKONGHMKMHEDA 180
OY	133	-----GSRGPAGH-----SEAG 145
DB	181	YYSEVKPLSPAFKPSADYHSHDLSTKPSYSDLKWGYQAASSPLDYEQFTFPSTA 240
OY	146	GSGGDRRA-----GP-----EKRPKSRESGGGFOESSRDKRPLSGPDVGT-OPA 191
DB	241	GTSGGSKESLIAYSEGEWGPSLDYDRLRRKSSYLNOTSPQPTR-ORRSRSGSGLDEPMMP 299
OY	192	GLASAKLAARPNVTY-----PADTDH-----PSRGAQGEPHDVAAPGP 232
DB	300	GASAKTNHPGHSTSYNTYTPRLSEPWCITPYVDYDRAOMVLSPILSG-----DTYPGP 354
OY	233	SAGGLAIPOS-----SSSSSRPPTRAKAPSFGVLGNHASPOLAPACTP----- 278
DB	355	A-----KLPGQSGKSGYSSSHQYPSGVNKA-----TLVNHPLQSSQYISTASYLSL 406
OY	279	AAPAVGPPGRRSPQRFQVSHQGFRAALDLYVDGPPRYSLDNFIKGESTIVICIA 338
DB	407	SSSTYPPSPWSGSSSQOQPSRVSHQGFRAALDLYVDPGPREYLAIFIKIGESTIVICIA 466

QY 339 TVSSGKLVAVKKMDLRKQORELLFNEVYIMRDYOHENVYEMNSYLVDGLVMVMEFL 398  
 Db 467 TEKHTGQVAVKKMDLRKQORELLFNEVYIMRDYOHENVYEMNSYLVDGLVMVMEFL 526  
 QY 399 EGALTDIVTHTRNNEEQIAVCLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVGLSD 458  
 Db 527 EGALTDIVTHTRNNEEQIAVCLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVGLSD 586  
 QY 459 FGFCAQVSKVPRKSLVGTPTWMAPELISRLPYGPEVDIWSLGINVIMVNDGEPPEYNE 518  
 Db 587 FGFCAQVSKVPRKSLVGTPTWMAPELISRLPYGPEVDIWSLGINVIMVNDGEPPEYNE 646  
 QY 519 PPLKAMKMRDNLPRLLKHLHVSPLSGFLDLRLVDPDPAORATAELLKHPFLAKAGRP 578  
 Db 647 PPLQAMRRIRDSLPPEVKDLHKSIVLKGFLDLMLVREPSQRAIODELGHFFLKLAGRP 706  
 QY 579 ASIVPLMRQNR 589  
 Db 707 SCIVPLMRQYR 717

RESULT 15  
 Q8TB93  
 ID 08TB93 PRELIMINARY; PRT; 719 AA.  
 AC 08TB93;  
 DT 01-JUN-2002 (TEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
 DE P21-activated kinase 7.  
 OS Name=PAK7; GN  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,  
 RA Diatchenko L., Manisala K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedln T.B., Toshiyuki S., Carninci P., Pangue C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,  
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalek U., Smalhev D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Matra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RL Strausberg R.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, BC024179; AAH24179.1; -.  
 DR HSSP, Q13153; 1F3M.  
 DR GO; GO:0005524; P:ATP binding; IEA.  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR011009; Kinase\_Like.  
 DR InterPro; IPR000095; PAKbox/Rhodning.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.

DR InterPro; IPR011026; WASP\_C.  
 DR Pfam; PF00786; PBD; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00285; PBD; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS0108; CRIB; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 KW ATP-binding; Kinase.  
 SQ SEQUENCE 719 AA; 80794 MW; 536CB5DE65DA9FC3 CRC64;

Query Match 56.0%; Score 1731; DB 2; Length 719;  
 Best Local Similarity 52.4%; Pred. No. 2, 7e-56;  
 Matches 383; Conservative 66; Mismatches 126; Indels 156; Gaps 17;

QY 1 MFGRKRKRVVISAPSNFHRVHTGPDQHQKFTGLPRQWOSLIESARPKPLVDPACIT 60  
 Db 1 MFGRKKKKKIEISGPSNFEHRVHTGPDQHQKFTGLPRQWOSLIESARPKPLVDPACIT 60  
 QY 61 SIOPGAPKTIYNGSKAKDGLTLLIDFENMSYTRNSLRDSDPPPPARA-----R 112  
 Db 61 SIOPGAPKTIYNGSKAKDGLTLLIDFENMSYTRNSLRDSDPPPPARA-----R 112  
 QY 113 QENGM-----PEEPATTA-----RGQ-----PGKA 132  
 Db 121 EENGFTTFSQYSESSTITADYTTETKREKSLYGDDLPYTRGSHAAKONGHVMKMGGA 180  
 QY 133 -----GSRGRFAGH-----SEAG 145  
 Db 181 YSEVVKPLKSDFAFADYHSHLDSLKPSEYSDLKWEYQRASSSSPLDYSFQFTSRRTA 240  
 QY 146 GSGGRRRA-----GP-----EKRPSSREGSGGPPESRDKRPPLSGPDVGT- 191  
 Db 241 GTSGSKESLASESEMGSLDDYDRPKSYLNQTSPOPTWR-QRSRSGSGLEPMPBF 299  
 QY 192 GLASGAKLAGRPNTY-----PRADTDH-----PSGAQGEPRHDVAPNGP 232  
 Db 300 GASAFPTHQGHSTSYTPRLSEPTWCIPKVDYDRAQNVLSPPLSGS-----DTYPRGP 354  
 QY 233 SAGGLAIPQS-----SSSSSRPTPRARGAPSPGVLGPAASPOLAPACTP----- 278  
 Db 355 A-----KLPSQSKSGVSSSHQYPSGVNKA-----TLNHPSLQSSSQYISTASYLSYLSL 406  
 QY 279 AAPAVDPGPPGPPSPQREPPRVSHQFRALQLVDPDGRSTYLDNFTIKIGSGTGIVCTA 338  
 Db 407 SSSYPPSPSGSSSQQPPSRVSHQFRALQLVSPDGRREVLANFIKIGSGTGIVCTA 466  
 QY 339 TVSSGKLVAVKKMDLRKQORELLFNEVYIMRDYOHENVYEMNSYLVDGLVMVMEFL 398  
 Db 467 TEKHTGQVAVKKMDLRKQORELLFNEVYIMRDYOHENVYEMNSYLVDGLVMVMEFL 526  
 QY 399 EGALTDIVTHTRNNEEQIAVCLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVGLSD 458  
 Db 527 EGALTDIVTHTRNNEEQIAVCLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVGLSD 586  
 QY 459 FGFCAQVSKVPRKSLVGTPTWMAPELISRLPYGPEVDIWSLGINVIMVNDGEPPEYNE 518  
 Db 587 FGFCAQVSKVPRKSLVGTPTWMAPELISRLPYGPEVDIWSLGINVIMVNDGEPPEYNE 646  
 QY 519 PPLKAMKMRDNLPRLLKHLHVSPLSGFLDLRLVDPDPAORATAELLKHPFLAKAGRP 578  
 Db 647 PPLQAMRRIRDSLPPEVKDLHKSIVLKGFLDLMLVREPSQRAIODELGHFFLKLAGRP 706  
 QY 579 ASIVPLMRQNR 589  
 Db 707 SCIVPLMRQYR 717

Search completed: March 15, 2005, 11:30:27  
 Job time : 204.897 secs

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GenCore version 5.1.6  
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OM protein - protein search, using bw model

Run on: March 15, 2005, 10:56:56 ; Search time 203.374 Seconds  
(without alignments)  
1123.919 Million cell updates/sec

Title: US-10-693-367-2

Perfect score: 3090

Sequence: 1 MGKKKKRVEISAPSNFHR.....LAKGPPASIVPLMRNRR 591

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*\*\*  
2: geneseqp1990s:\*\*\*  
3: geneseqp2000s:\*\*\*  
4: geneseqp2001s:\*\*\*  
5: geneseqp2002s:\*\*\*  
6: geneseqp2003as:\*\*\*  
7: geneseqp2003bs:\*\*\*  
8: geneseqp2004s:\*\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3090	100.0	591	2	AAVS5964
2	3090	100.0	591	3	AAVS9128
3	3090	100.0	591	7	ADCS7307
4	3090	100.0	591	7	ADDB9973
5	3090	100.0	591	7	ADFA5079
6	3090	100.0	591	8	ADH23362
7	3090	100.0	591	8	ABM62101
8	3090	100.0	620	4	ABG19308
9	3075	99.5	588	4	ADH23359
10	2860	92.6	593	8	ADJ96654
11	2674.5	86.6	522	8	ABM84642
12	2674.5	86.6	522	8	ABM84644
13	2674.5	86.6	522	8	ABM84645
14	2662	86.1	517	8	ABM84648
15	2662	86.1	517	8	ABM84647
16	2662	86.1	517	8	ABM84643
17	2662	86.1	517	8	ABM84646
18	2558	82.8	501	7	ADCS7309
19	2202.5	71.3	438	7	ADCS7305
20	2194.5	71.0	438	8	ADRS9753
21	2073	67.1	398	2	AAVS5941
22	1748	56.6	719	7	ADJ83007
23	1739	56.3	719	7	ADJ83008
24	1734	56.1	719	4	AAVS8963
25	1731	56.0	719	4	AAVS5705

26	1731	56.0	719	7	ADCS7451	Adc37451 Nuclear f
27	1731	56.0	719	7	ADFA5080	Adfa5080 Human kin
28	1731	56.0	719	8	AD129314	Ad129314 Human MAR
29	1730	56.0	719	4	AAE02187	AAe02187 Human p21
30	1549	50.1	457	8	ADH42207	Adh42207 Novel hum
31	1549	50.1	457	8	ADH42215	Adh42215 Novel hum
32	1549	50.1	457	8	ADH42217	Adh42217 Novel hum
33	1545	50.0	457	8	ADH42213	Adh42213 Novel hum
34	1535	49.7	457	8	ADH42211	Adh42211 Novel hum
35	1502	48.6	293	7	ADH15851	Adh15851 PKA4D pr
36	1497.5	48.5	639	8	ADH23364	Adh23364 Fruit fly
37	1494.5	48.4	635	8	ADH23360	Adh23360 Fruit fly
38	1473.5	47.7	681	2	AAVS5940	AAVS5940 Human PAK
39	1473.5	47.7	681	4	AAE03357	AAE03357 Signal tr
40	1473.5	47.7	681	4	AAE20337	AAE20337 Human PAK
41	1473.5	47.7	681	5	ABP64709	ABP64709 Human pro
42	1473.5	47.7	681	8	ADQ15150	ADq15150 Human can
43	1473.5	47.7	701	6	ABU11508	ABu11508 Human MDP
44	1470.5	47.6	681	3	AAE03970	AAE03970 Mutant s1
45	1470.5	47.6	681	4	AAE63230	AAe63230 Amino aci

#### ALIGNMENTS

RESULT 1  
ID AAVS5964 standard; protein; 591 AA.  
AC AAVS5964;  
XX  
XX  
DT 18-FEB-2000 (first entry)  
XX  
DE Full length human PAKs protein.  
XX  
XX Antithematic; antiatheritic; antiinflammatory; antiallergic; osteopathic;  
KM Antipsoptic; antiarteriosclerotic; antiaschemic; immunosuppressive;  
KM neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic;  
KM Vlnery; STE20; protein kinase; STK2; STK3; STK4; STK5; STK6; STK7;  
KM ZC1; ZC2; ZC3; ZC4; KHS2; SULU1; SULU2; GSK2; STK4; PAK5; antagonistic;  
KM antibody; gene therapy; rheumatoid arthritis; arteriosclerosis; asthma;  
KM inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;  
KM rhinitis; autoimmunity; organ transplantation; multiple sclerosis;  
KM myocardial infarction; cardiovascular disease; stroke; renal failure;  
KM oxidative stress-related neurodegenerative disorder; Parkinson's disease;  
KM amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;  
KM ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;  
KM mesangial disorder; growth regulation; wound healing; T cell activation;  
KM immunosuppressant.  
XX  
XX Homo sapiens.  
OS  
XX WO9953036-A2.  
XX  
XX 21-OCT-1999.  
XX  
XX 13-APR-1999; 99WO-US008150.  
XX  
XX 14-APR-1998; 98US-0081784P.  
XX  
XX (SUGB-) SUGEN INC.  
XX  
XX Plowman G, Martinez R, Whyte D;  
XX  
XX WPI; 1999-611301/52.  
XX  
XX N-PSDB; AA240538.  
XX  
XX Novel kinase-related polypeptides used for the diagnosis and treatment of  
PT kinase-related diseases and disorders.  
XX  
XX Claim 11; Page 366-368; 387pp; English.  
XX  
XX This sequence represents a novel STE20-related protein kinase. The

invention relates to nucleic acid molecule encoding a kinase polypeptide selected from STK2, STK3, STK4, STK5, STK6, STK7, ZC1, ZC2, ZC3, ZC4, KHS2, SUN1, SUN3, GSK3, PAK4 and PAK5. The proteins are used to identify agonists and antagonists, and to raise antibodies. The polynucleotides are useful in gene therapy protocols. The polynucleotides, polypeptides, antibodies, antagonists and agonists may be used to treat diseases such as immune-related disorders and diseases (e.g. rheumatoid arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g. Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis, rhinitis, autoimmunity, and organ transplantation, chronic inflammatory disease, multiple sclerosis, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders (e.g. amyotrophic lateral sclerosis, Parkinson's disease and Leigh syndrome), cancer, cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes mellitus, fibrotic and mesangial disorders. The proteins may also be useful for cell growth regulation (e.g. in wound healing), T cell activation, mitosis control, and as immunosuppressants

Sequence 591 AA;

Query Match 100.0%; Score 3090; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 2.8e-216;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MFGKRRKVEISAPSNFHRVHTGPDHOKFTGLPRQMSLIESARPKPLVDPACIT 60
DB 1 MFGKRRKVEISAPSNFHRVHTGPDHOKFTGLPRQMSLIESARPKPLVDPACIT 60
QY 61 SIOPGAPKTIYVSGSKAGDGLTLLDEFENMSVTRNSLRDSDPPPARAOGEMPEE 120
DB 61 SIOPGAPKTIYVSGSKAGDGLTLLDEFENMSVTRNSLRDSDPPPARAOGEMPEE 120
QY 121 PATTARGGPGKAGSRGFRAGHSEAGGSGDRRAGRRPKSRSGSGPOSSSRDKRPL 180
DB 121 PATTARGGPGKAGSRGFRAGHSEAGGSGDRRAGRRPKSRSGSGPOSSSRDKRPL 180
QY 181 SGPDVGTQPGAGLASGAKLAAGRPFNTYPRADTHPSRGAQGEPHDVAENGSAAGLAIP 240
DB 181 SGPDVGTQPGAGLASGAKLAAGRPFNTYPRADTHPSRGAQGEPHDVAENGSAAGLAIP 240
QY 241 QSSSSSSRPPTARAGSPGVLGPHASEPOLAPACTPAAPAVPGPPRSPQREPORVS 300
DB 241 QSSSSSSRPPTARAGSPGVLGPHASEPOLAPACTPAAPAVPGPPRSPQREPORVS 300
QY 301 HEQFRAALQLVVDPPDRSYLDNFKIGSGTGIVCIATVRSSGKLVAVKMDLRKQQR 360
DB 301 HEQFRAALQLVVDPPDRSYLDNFKIGSGTGIVCIATVRSSGKLVAVKMDLRKQQR 360
QY 361 ELLFNEVVMIRDYOHENNVEMTNSYLVDGLVWMEFLEGALTDIVTTRANNEQIAAV 420
DB 361 ELLFNEVVMIRDYOHENNVEMTNSYLVDGLVWMEFLEGALTDIVTTRANNEQIAAV 420
QY 421 CLAIVQALSVLHAQGVYHDIKSDSILLTHDRVKLSDFGCAQVSKVPRKRSIVGTPT 480
DB 421 CLAIVQALSVLHAQGVYHDIKSDSILLTHDRVKLSDFGCAQVSKVPRKRSIVGTPT 480
QY 481 WMAPELISRLPYGPEVDIWSLGIWVEMWDGSPFVNEBPPLKAMKTIKRNLPRLKNLKK 540
DB 481 WMAPELISRLPYGPEVDIWSLGIWVEMWDGSPFVNEBPPLKAMKTIKRNLPRLKNLKK 540
QY 541 VSPSLKGLFRLRLVNDPAQATAAELLKHPFLAKAGPPASIVPLMKRONTR 591
DB 541 VSPSLKGLFRLRLVNDPAQATAAELLKHPFLAKAGPPASIVPLMKRONTR 591

```

RESULT 2  
AA59128  
ID AA59128 standard; protein; 591 AA.  
XX AA59128;  
AC  
XX  
DT 08-MAR-2000 (first entry)

Human serine/threonine kinase, PAK4.  
PAK4; serine/threonine kinase; GTPase; intracellular signal cascade; Rac; Cdc42H; morphogenesis; mitogenesis; JNK; p38 MAP kinase; human; actin polymerization; filopodia; cancer; arthritis.  
Homo sapiens.  
W09963073-A1.  
09-DEC-1999.  
21-MAY-1999; 99MO-US011341.  
21-MAY-1998; 98US-00082737.  
(UYCO ) UNIV COLUMBIA NEW YORK.  
Minden A;  
WPI, 2000-072881/06.  
N-PSDB; AA240657.  
Novel mammalian nucleic acid useful for treating cancer and arthritis.  
Claim 6; Fig 1A-B; 95pp; English.

The invention relates to an isolated mammalian nucleic acid that encodes PAK4, a novel serine/threonine kinase or its mutant homolog. PAK4 is an effector for the GTPases Rac and Cdc42Hs which are involved in intracellular signal cascades, morphogenesis and mitogenesis, and activate the JNK and p38 MAP kinase pathways. Inhibiting interaction of PAK4 with these enzymes will thus result in inhibition of actin polymerization and formation of filopodia. The PAK4 nucleic acid used for recombinant production of the protein, and as a source of probes for identifying homologous sequences and of (anti)sense oligonucleotides for inhibiting PAK4 expression. The protein, or its fragments, are used to raise specific antibodies and these are useful as ligands for therapeutic inhibition of interaction between PAK4 and its native binding partners. Inhibition of PAK4 activity or expression is used for treatment of cancer and arthritis. The present sequence represents the human serine/threonine kinase, PAK4

Sequence 591 AA;

Query Match 100.0%; Score 3090; DB 3; Length 591;  
Best Local Similarity 100.0%; Pred. No. 2.8e-216;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MFGKRRKVEISAPSNFHRVHTGPDHOKFTGLPRQMSLIESARPKPLVDPACIT 60
DB 1 MFGKRRKVEISAPSNFHRVHTGPDHOKFTGLPRQMSLIESARPKPLVDPACIT 60
QY 61 SIOPGAPKTIYVSGSKAGDGLTLLDEFENMSVTRNSLRDSDPPPARAOGEMPEE 120
DB 61 SIOPGAPKTIYVSGSKAGDGLTLLDEFENMSVTRNSLRDSDPPPARAOGEMPEE 120
QY 121 PATTARGGPGKAGSRGFRAGHSEAGGSGDRRAGRRPKSRSGSGPOSSSRDKRPL 180
DB 121 PATTARGGPGKAGSRGFRAGHSEAGGSGDRRAGRRPKSRSGSGPOSSSRDKRPL 180
QY 181 SGPDVGTQPGAGLASGAKLAAGRPFNTYPRADTHPSRGAQGEPHDVAENGSAAGLAIP 240
DB 181 SGPDVGTQPGAGLASGAKLAAGRPFNTYPRADTHPSRGAQGEPHDVAENGSAAGLAIP 240
QY 241 QSSSSSSRPPTARAGSPGVLGPHASEPOLAPACTPAAPAVPGPPRSPQREPORVS 300
DB 241 QSSSSSSRPPTARAGSPGVLGPHASEPOLAPACTPAAPAVPGPPRSPQREPORVS 300
QY 301 HEQFRAALQLVVDPPDRSYLDNFKIGSGTGIVCIATVRSSGKLVAVKMDLRKQQR 360
DB 301 HEQFRAALQLVVDPPDRSYLDNFKIGSGTGIVCIATVRSSGKLVAVKMDLRKQQR 360

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QY 361 ELLFNEVIMRDYQHENVEMNYSYVGDELWVMEFLGALTDIVTHTRNMEEOIAAV 420
DB 361 ELLFNEVIMRDYQHENVEMNYSYVGDELWVMEFLGALTDIVTHTRNMEEOIAAV 420
QY 421 CLAVALQALSVLHAQGYIHHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKSLVGTPE 480
DB 421 CLAVALQALSVLHAQGYIHHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKSLVGTPE 480
QY 481 WMAPELISRLPYGPEVDIWSLGIWIEWDGEPYPNEPPLKAMKMI RNLPPRLKNLHK 540
DB 481 WMAPELISRLPYGPEVDIWSLGIWIEWDGEPYPNEPPLKAMKMI RNLPPRLKNLHK 540
QY 541 VSPSLKGFIDRLILVRDPAQRATPAELLKHPFLAKAGPPASIVPLMKONRTR 591
DB 541 VSPSLKGFIDRLILVRDPAQRATPAELLKHPFLAKAGPPASIVPLMKONRTR 591

RESULT 3
ID ADC37307 standard; protein; 591 AA.
AC ADC37307;
XX
XX 18-DEC-2003 (first entry)
DT
DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 140.
XX
XX
XX Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
XX cancer; infectious disease; bone disease; AIDS;
XX neurodegenerative disease; ischemic disorder; Antinflammatory;
XX Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
XX Neuroprotective; Nootropic; Cardiant; Gene therapy; human.
XX
XX Homo sapiens.
XX
XX MO2003048202-A2.
XX
XX 12-JUN-2003.
XX
XX
XX 03-DEC-2002; 2002WO-JP012644.
XX
XX
XX 03-DEC-2001; 2001JP-00368692.
XX
XX 05-DEC-2001; 2001US-0335829P.
XX
XX 03-OCT-2002; 2002JP-00291302.
XX
XX 04-OCT-2002; 2002US-0415769P.
XX
XX
XX (ASAH ) ASAMI KASEI KK.
XX
XX
XX Matouda A, Muramatsu S;
XX
XX
XX WPI; 2003-505282/47.
XX
XX N-PSDB; ADC37306.
XX
XX
XX
XX New purified protein that activates nuclear factor kappa B (NF-kappaB),
XX useful for treating inflammation, autoimmune diseases, cancer,
XX infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
XX ischemic disorders.
XX
XX
XX Claim 1; SEQ ID NO 140; 938pp; English.
XX
XX
XX
XX The present invention relates to novel proteins and their coding
XX sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
XX kappaB). The proteins and their coding sequences are useful for treating
XX a disease associated with NF-kappaB activation, such as inflammation,
XX autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
XX neurodegenerative diseases, or ischemic disorders.
XX
XX
XX Sequence 591 AA;
XX
XX
XX Query Match 100.0%; Score 3090; DB 7; Length 591;
XX Best local Similarity 100.0%; Pred. No. 2,8e-216;
XX Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 MFGKKRKRVEISAPSNFEHRVHTGPDHOKFTGLPRQWOSLIIESARRPKPLVDPACIT 60
DB 1 MFGKKRKRVEISAPSNFEHRVHTGPDHOKFTGLPRQWOSLIIESARRPKPLVDPACIT 60
QY 61 SIOPGAPKTIIVGSKAKGALTLILDEFENNSVTRSNLSLRDPPPPARARQENGMPEE 120
DB 61 SIOPGAPKTIIVGSKAKGALTLILDEFENNSVTRSNLSLRDPPPPARARQENGMPEE 120
QY 121 PATTARAGPGKAGSRGFRFGHSEBAGGSGDRRRAPGEKPKSKSREGSGGPOESSRKRPL 180
DB 121 PATTARAGPGKAGSRGFRFGHSEBAGGSGDRRRAPGEKPKSKSREGSGGPOESSRKRPL 180
QY 181 SGPDVGTTPQAGIASAKIILAAGRPFTYPRATDHSRGAQSBPHVAANGSAGGLAIP 240
DB 181 SGPDVGTTPQAGIASAKIILAAGRPFTYPRATDHSRGAQSBPHVAANGSAGGLAIP 240
QY 241 QSSSSSRPPTARAGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPGRSPQREPORVS 300
DB 241 QSSSSSRPPTARAGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPGRSPQREPORVS 300
QY 301 HEQFRAALQLVDPGDPRSYLDNFIKIGEGSTGIVCIATVRSKGKLVAVKMDLRKQORR 360
DB 301 HEQFRAALQLVDPGDPRSYLDNFIKIGEGSTGIVCIATVRSKGKLVAVKMDLRKQORR 360
QY 361 ELLFNEVIMRDYQHENVEMNYSYVGDELWVMEFLGALTDIVTHTRNMEEOIAAV 420
DB 361 ELLFNEVIMRDYQHENVEMNYSYVGDELWVMEFLGALTDIVTHTRNMEEOIAAV 420
QY 421 CLAVALQALSVLHAQGYIHHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKSLVGTPE 480
DB 421 CLAVALQALSVLHAQGYIHHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKSLVGTPE 480
QY 481 WMAPELISRLPYGPEVDIWSLGIWIEWDGEPYPNEPPLKAMKMI RNLPPRLKNLHK 540
DB 481 WMAPELISRLPYGPEVDIWSLGIWIEWDGEPYPNEPPLKAMKMI RNLPPRLKNLHK 540
QY 541 VSPSLKGFIDRLILVRDPAQRATPAELLKHPFLAKAGPPASIVPLMKONRTR 591
DB 541 VSPSLKGFIDRLILVRDPAQRATPAELLKHPFLAKAGPPASIVPLMKONRTR 591

RESULT 4
ID ADD89973 standard; protein; 591 AA.
AC ADD89973;
XX
XX 29-JAN-2004 (first entry)
DT
DE Human cancer-associated protein kinase PAK4.
XX
XX
XX PAK4; protein kinase; enzyme; cancer; cytosolic; immunosuppressive;
XX antidiabetic; antirheumatic; antiarthritic; antipsoriatic;
XX antiangiogenic; antiarteriosclerotic; antiinflammatory; vulnery;
XX gynaecological; neuroprotective; gene therapy; human.
XX
XX
XX Homo sapiens.
XX
XX
XX MO2003083096-A2.
XX
XX
XX 09-OCT-2003.
XX
XX 21-MAR-2003; 2003WO-CA000409.
XX
XX 28-MAR-2002; 2002US-0368853P.
XX
XX
XX (KINE-) KINETEK PHARM INC.
XX
XX
XX Delaney AD;
XX
XX
XX WPI; 2003-833542/77.
XX
XX N-PSDB; ADD89972.

```

XX New nucleic acids encoding cancer associated protein kinases, useful as  
PT targets for screening pharmaceutical agents that inhibit the growth of  
PT tumor cells, or for diagnosing and treating cancer, inflammation or  
PT autoimmune disease.

PS Claim 1, Page 77-78; 91pp; English.

CC The present sequence is the protein sequence of human cancer-associated  
CC protein kinase, PAK4. PAK-related kinase PAK4 is an effector molecule for  
CC Cdc42h. Its gene expression is up-regulated in cancers of the brain,  
CC lung, muscle and uterus. PAK4 is one of a set of protein kinases that are  
CC shown by the invention to be over-expressed in hyper-proliferative cells.  
CC These protein kinases provide targets for drug screening for agents  
CC effective in inhibiting the growth or metastasis of tumour cells, and for  
CC determining other molecular targets in kinase signal transduction  
CC pathways involved in transformation and growth of tumour cells. A claimed  
CC method for inhibiting the growth of a cancer cell involves down-  
CC regulating the activity of the protein kinase using an antisense sequence  
CC or inhibitor of kinase activity, especially where the cancer cell is a  
CC breast, liver, colon, muscle, prostate, kidney, lung, placental or  
CC uterine cancer cell. Detection of over-expression in cancers provides a  
CC useful diagnostic for predicting patient prognosis and probability of  
CC drug effectiveness. Agents that specifically bind the protein kinases can  
CC be used for treatment and visualisation of tumours in patients. The  
CC protein kinase polypeptides and nucleic acids may also be used for  
CC treating hyperproliferative diseases, such as autoimmune disease,  
CC diabetes mellitus, multiple sclerosis, rheumatoid arthritis, psoriasis,  
CC atherosclerosis, inflammation, scarring, endometriosis and angiogenesis.

XX Sequence 591 AA;

Query Match 100.0%; Score 3090; DB 7; Length 591;

Best Local Similarity 100.0%; Pred. No. 2.8e-216; Indels 0; Gaps 0;

Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGKRRKRVETISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIESARPRKPLVPACIT 60  
DB 1 MFGKRRKRVETISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIESARPRKPLVPACIT 60  
QY 61 SIOPGAPKTIYRSGSKAGDGLTLLDDEFENMSVTRSNLSLRDSDPPPARARQENGMPRE 120  
DB 61 SIOPGAPKTIYRSGSKAGDGLTLLDDEFENMSVTRSNLSLRDSDPPPARARQENGMPRE 120  
QY 121 PATTARGGPGKAGRGFRFAGHSEAGGSGDRRRAGPEKRPKSRSGSGPQESSSRDKRPL 180  
DB 121 PATTARGGPGKAGRGFRFAGHSEAGGSGDRRRAGPEKRPKSRSGSGPQESSSRDKRPL 180  
QY 181 SGPDVGTQPGAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGSAGGLAIP 240  
DB 181 SGPDVGTQPGAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGSAGGLAIP 240  
QY 241 QSSSSSSRPPTARAGAPSPGVLGPHASBPQLAPACTPPAABAVPGPGRSPQREBPQRVS 300  
DB 241 QSSSSSSRPPTARAGAPSPGVLGPHASBPQLAPACTPPAABAVPGPGRSPQREBPQRVS 300  
QY 301 HEQFPAALQLVVDPGPPRSYTLNFKIKIGSGTICIAIVTRSSGKLVAVKMDLAKQOR 360  
DB 301 HEQFPAALQLVVDPGPPRSYTLNFKIKIGSGTICIAIVTRSSGKLVAVKMDLAKQOR 360  
QY 361 ELLFNEVIMRDYQEHNVEMTNSYLVDGLVWVEFLGALTDIVTHTRNNEQIAAV 420  
DB 361 ELLFNEVIMRDYQEHNVEMTNSYLVDGLVWVEFLGALTDIVTHTRNNEQIAAV 420  
QY 421 CLAIVQALSVLHAQGVIRHDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGT 480  
DB 421 CLAIVQALSVLHAQGVIRHDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGT 480  
QY 481 WMAPELISRLPYGPEVDIWSLGIWVTEMVDGEPVFNBPBLKAMKIMIDNLPRLKLNHK 540  
DB 481 WMAPELISRLPYGPEVDIWSLGIWVTEMVDGEPVFNBPBLKAMKIMIDNLPRLKLNHK 540  
QY 541 VSPSLKGFIDRLVLVDPQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591

DB 541 VSPSLKGFIDRLVLVDPQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591

RESULT 5  
ADP45079 standard; protein; 591 AA.

ADP45079;

12-FEB-2004 (first entry)

Human kinase PAK4.

Human; protein kinase; enzyme; inhibitor; PAK4.

Homo sapiens.

WO2003081210-A2.

02-OCT-2003.

20-MAR-2003; 2003WO-US008725.

21-MAR-2002; 2002US-036682P.

(SUNBE-) SUNESIS PHARM INC.

Prescott JC, Braisted A;

WPI; 2003-865136/80.

PT Identifying ligand binding to inactive conformation of target protein  
PT kinase (T) comprises contacting the conformation modified (T) which  
PT contains reactive group at binding site, with ligands and detecting  
PT kinase-ligand conjugate formation.

Disclosure; SEQ ID NO 48; 260pp; English.

CC The present invention relates to a method for identifying a ligand (L),  
CC which binds to an inactive conformation of target protein kinase (T). The  
CC method involves contacting inactive conformation of (T), which contains  
CC or is modified to contain a reactive group at or near a binding site of  
CC interest, with one or more ligand candidates capable of covalently  
CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).  
CC The method is useful for identifying protein kinase inhibitors that  
CC preferentially bind to inactive conformation of a target protein kinase.  
CC The present sequence is a protein kinase which may be modified via an  
CC amino acid substitution, for use in the method of the invention.

XX Sequence 591 AA;

Query Match 100.0%; Score 3090; DB 7; Length 591;

Best Local Similarity 100.0%; Pred. No. 2.8e-216; Indels 0; Gaps 0;

Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGKRRKRVETISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIESARPRKPLVPACIT 60  
DB 1 MFGKRRKRVETISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIESARPRKPLVPACIT 60  
QY 61 SIOPGAPKTIYRSGSKAGDGLTLLDDEFENMSVTRSNLSLRDSDPPPARARQENGMPRE 120  
DB 61 SIOPGAPKTIYRSGSKAGDGLTLLDDEFENMSVTRSNLSLRDSDPPPARARQENGMPRE 120  
QY 121 PATTARGGPGKAGRGFRFAGHSEAGGSGDRRRAGPEKRPKSRSGSGPQESSSRDKRPL 180  
DB 121 PATTARGGPGKAGRGFRFAGHSEAGGSGDRRRAGPEKRPKSRSGSGPQESSSRDKRPL 180  
QY 181 SGPDVGTQPGAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGSAGGLAIP 240  
DB 181 SGPDVGTQPGAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGSAGGLAIP 240  
QY 241 QSSSSSSRPPTARAGAPSPGVLGPHASBPQLAPACTPPAABAVPGPGRSPQREBPQRVS 300



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XX  MPI: 2004-347921/32.
DR  N-PSDB; ACN40564.
XX
PT  New tumor-associated antigenic target polypeptides and nucleic acids,
PT  useful in preparing a medicament for treating or detecting a
PT  proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT  prostate cancer or tumor.
XX
PS  Claim 12; SEQ ID NO 5422; 7273bp; English.
XX
CC  The invention relates to human tumour-associated antigenic target (TAT)
CC  polypeptides, and their related nucleic acids. The TAT polypeptides are
CC  overexpressed in cancer tissues compared to normal tissues, and may thus
CC  serve as effective targets for the diagnosis and treatment of cancer in
CC  mammals. The invention also relates to nucleic acid and polypeptide
CC  sequences at least 80% identical to the TAT nucleic acids and
CC  polypeptides; expression vectors and host cells comprising a TAT nucleic
CC  acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC  molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC  TAT polypeptide; and methods and compositions for the treatment or
CC  diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC  antibodies, antagonists, binding molecules and compositions are useful
CC  for diagnosing or treating a cell proliferative disorder associated with
CC  increased TAT expression, particularly cancers such as breast cancer,
CC  colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC  cancer, pancreatic cancer, cervical cancer, cancers of the central
CC  nervous system, melanoma and leukemia. TAT nucleic acids may further be
CC  used as hybridisation probes, in chromosome and gene mapping, in
CC  chromosome identification and in gene therapy. The present sequence
CC  represents a TAT polypeptide of the invention
XX
SQ  Sequence 591 AA;

Query Match      100.0%; Score 3090; DB 8; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.8e-216;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  MFGKKRKRVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIESARRPKLVDPACT 60
DB  1  MFGKKRKRVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIESARRPKLVDPACT 60

QY  61  SIQCAPKTIIVGSKGAKDGLATLLIDFEENSVTRNSLRDSDPPPARAQENGMEE 120
DB  61  SIQCAPKTIIVGSKGAKDGLATLLIDFEENSVTRNSLRDSDPPPARAQENGMEE 120

QY  121  PATTARGPGRKAGSGRFRAGSEAGGSGDRRARAPKPKSRGSGGSGGPOSSSDKRL 180
DB  121  PATTARGPGRKAGSGRFRAGSEAGGSGDRRARAPKPKSRGSGGSGGPOSSSDKRL 180

QY  181  SGPVGTGPQAGLAGAKLAAGRPNFTYPRADTDHPSRGAQGEPRHDVAPNGSAGALAI 240
DB  181  SGPVGTGPQAGLAGAKLAAGRPNFTYPRADTDHPSRGAQGEPRHDVAPNGSAGALAI 240

QY  241  QSSSSSSRPPTARAGSPGVIGPAASEPQOLAPACTPAAPAVPQPPGRSPQRPQVS 300
DB  241  QSSSSSSRPPTARAGSPGVIGPAASEPQOLAPACTPAAPAVPQPPGRSPQRPQVS 300

QY  301  HEQPPAALQLVDPDPRSYLDNFKIGEGSTGIVCIATVSSSGTLVAVKKMDLKKQRR 360
DB  301  HEQPPAALQLVDPDPRSYLDNFKIGEGSTGIVCIATVSSSGTLVAVKKMDLKKQRR 360

QY  361  ELLFNEVIMEDYQHENVEMTNSYLVDGLVWVEFEGGALTJIVHTRNNEQIAY 420
DB  361  ELLFNEVIMEDYQHENVEMTNSYLVDGLVWVEFEGGALTJIVHTRNNEQIAY 420

QY  421  CLAVIQALSVLHAQGVIRHDIKSDSILLTHDGRVLTSDFGCAQVSKVPRKSLVGT 480
DB  421  CLAVIQALSVLHAQGVIRHDIKSDSILLTHDGRVLTSDFGCAQVSKVPRKSLVGT 480

QY  481  WMAPELISRLPYGPEVDIWSIGIMTIEWVDGEPFENRPPPLKAMKMTIDNLPRLK 540
DB  481  WMAPELISRLPYGPEVDIWSIGIMTIEWVDGEPFENRPPPLKAMKMTIDNLPRLK 540

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QY  541  VSPSLKGFUDRLVDPAPORATTAELLKHPPLAKGPPASIVPLMRQNR 591
DB  541  VSPSLKGFUDRLVDPAPORATTAELLKHPPLAKGPPASIVPLMRQNR 591

RESULT 8
ABG19308
ID  ABG19308 standard; protein; 620 AA.
XX
AC  ABG19308;
XX
DT  18-FEB-2002 (first entry)
XX
DE  Novel human diagnostic protein #19299.
XX
KW  Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW  food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS  Homo sapiens.
XX
PN  WO200175067-A2.
XX
PD  11-OCT-2001.
XX
PF  30-MAR-2001; 2001WO-US008631.
XX
PR  31-MAR-2000; 2000US-00540217.
XX  23-AUG-2000; 2000US-00649167.
XX
PA  (HYSE-) HYSEQ INC.
XX
PI  Dmanac RT, Liu C, Tang YT;
XX
DR  MPI: 2001-639362/73.
DR  N-PSDB; AAS83495.
XX
PT  New isolated polynucleotide and encoded polypeptides, useful in
PT  diagnostics, forensics, gene mapping, identification of mutations
PT  responsible for genetic disorders or other traits and to assess
PT  biodiversity.
XX
PS  Claim 20; SEQ ID NO 49667; 103bp; English.
XX
CC  The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC  sequences. (I) is useful as hybridisation probes, polymerase chain
CC  reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC  and in recombinant production of (II). The polynucleotides are also used
CC  in diagnostics as expressed sequence tags for identifying expressed
CC  genes. (I) is useful in gene therapy techniques to restore normal
CC  activity of (II) or to treat disease states involving (II). (II) is
CC  useful for generating antibodies against it, detecting or quantitating a
CC  polypeptide in tissue, as molecular weight markers and as a food
CC  supplement. (II) and its binding partners are useful in medical imaging
CC  of sites expressing (II). (I) and (II) are useful for treating disorders
CC  involving aberrant protein expression or biological activity. The
CC  polypeptide and polynucleotide sequences have applications in
CC  diagnostics, forensics, gene mapping, identification of mutations
CC  responsible for genetic disorders or other traits to assess biodiversity
CC  and to produce other types of data and products dependent on DNA and
CC  amino acid sequences. ABG00010-ABG10377 represent novel human diagnostic
CC  amino acid sequences of the invention. Note: The sequence data for this
CC  patent did not appear in the printed specification, but was obtained in
CC  electronic format directly from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 620 AA;

Query Match      100.0%; Score 3090; DB 4; Length 620;
Best Local Similarity 100.0%; Pred. No. 2.9e-216;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  MFGKKRKRVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIESARRPKLVDPACT 60

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Db      30 MGKRRKRVETISAPSNFEHRVHTGPDQHEQKFTGLPRQMSLIEESARRPKPLVDACIT 89
Qy      61 STPGAPKTIYVSGSKAKGALTLILDEFENNSVTSNSLRDSDPPPPARARQENGMPEE 120
Db      90 STPGAPKTIYVSGSKAKGALTLILDEFENNSVTSNSLRDSDPPPPARARQENGMPEE 149
Qy     121 PATTARAGGPKAGSRGFRFAGHSEAGGSGDRRRAAGEKPKSREGSGGPOESSRDKRPL 180
Db     150 PATTARAGGPKAGSRGFRFAGHSEAGGSGDRRRAAGEKPKSREGSGGPOESSRDKRPL 209
Qy     181 SGPDVGTPOGAGIAGAKLAAGRPFTYPRADTDHPSRGAQGEPHDVAENGPAGGLAIP 240
Db     210 SGPDVGTPOGAGIAGAKLAAGRPFTYPRADTDHPSRGAQGEPHDVAENGPAGGLAIP 269
Qy     241 QSSSSSSRPPTARAGAPSPGVIGPHASEPQLAPPAAPVAPGPPGRSPQREPORVS 300
Db     270 QSSSSSSRPPTARAGAPSPGVIGPHASEPQLAPPAAPVAPGPPGRSPQREPORVS 329
Qy     301 HEOFRALQLVDPGDPGRSYLNFITKIGSGTGVICIAVRSNGKLVAAKMDLRQQR 360
Db     330 HEOFRALQLVDPGDPGRSYLNFITKIGSGTGVICIAVRSNGKLVAAKMDLRQQR 389
Qy     361 ELLFNEVIMRDYOHENNVEMVNSYLVDLWVMEFLEGALTDIVTHRMNEEQIAAV 420
Db     390 ELLFNEVIMRDYOHENNVEMVNSYLVDLWVMEFLEGALTDIVTHRMNEEQIAAV 449
Qy     421 CLAVALQALSVLHAQGVYHDIKSDSITLTHDGRVKLSDFGCAQVSKEYVRRKSLVGTPE 480
Db     450 CLAVALQALSVLHAQGVYHDIKSDSITLTHDGRVKLSDFGCAQVSKEYVRRKSLVGTPE 509
Qy     481 WMAPELISRLPYGPEVDIWSLGIWVEMWDGEPYNEPPLKMKMIRDLNLPRLKNLHK 540
Db     510 WMAPELISRLPYGPEVDIWSLGIWVEMWDGEPYNEPPLKMKMIRDLNLPRLKNLHK 569
Qy     541 VSPSLKGFDRLLVDRDPAQRATAELKHPFLAKAGPPASIVPLMKQNTR 591
Db     570 VSPSLKGFDRLLVDRDPAQRATAELKHPFLAKAGPPASIVPLMKQNTR 620

RESULT 9
ADH23359
ID ADH23359 standard; protein; 588 AA.
XX
AC ADH23359;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human p21 (CDKN1A)-activated kinase 4 (PAK4) serine/threonine kinase #1.
XX
KW human; p21 (CDKN1A)-activated kinase 4; PAK4; serine/threonine kinase;
KM enzyme; HIV-Tat transcriptional activity.
XX
OS Homo sapiens.
XX
PN US2003186254-A1.
XX
PD 02-OCT-2003.
XX
PF 29-APR-2002; 2002US-00134102.
XX
PR 30-DEC-1999; 99US-0173939P.
XX
PR 28-DEC-2000; 2000US-00750457.
XX
PA (CELL-) CELL SIGNALING TECHNOLOGY INC.
XX
PI Melnick MB, Moritz A, Comb MJ;
XX
DR WPI; 2004-130707/13.
XX
DR N-PSDB; ADH23361.
XX
PT New isolated DNA sequence encoding PAK4 serine/threonine kinase for
modulating the transcriptional activity of human immunodeficiency virus-

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PT Tat protein.
XX
XX Claim 1; SEQ ID NO 1; 47bp; English.
XX
CC The invention relates to an isolated DNA sequence encoding p21 (CDKN1A)-
CC activated kinase 4 (PAK4) serine/threonine kinase. The invention is
CC useful for modulating the transcriptional activity of HIV-Tat protein.
CC The invention provides isolated DNA and vectors encoding PAK4 and Cdc42-
CC GEF which synergize to stimulate Tat transcriptional activity. The
CC present sequence represents the amino acid sequence of human PAK4.
XX
SQ Sequence 588 AA;
XX
Query Match          99.5%; Score 3075; DB 8; Length 588;
Best Local Similarity 100.0%; Pred. No. 3.4e-215;
Matches 588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 MGKRRKRVETISAPSNFEHRVHTGPDQHEQKFTGLPRQMSLIEESARRPKPLVDACIT 60
Db      1 MGKRRKRVETISAPSNFEHRVHTGPDQHEQKFTGLPRQMSLIEESARRPKPLVDACIT 60
Qy      61 STPGAPKTIYVSGSKAKGALTLILDEFENNSVTSNSLRDSDPPPPARARQENGMPEE 120
Db      61 STPGAPKTIYVSGSKAKGALTLILDEFENNSVTSNSLRDSDPPPPARARQENGMPEE 120
Qy      121 PATTARAGGPKAGSRGFRFAGHSEAGGSGDRRRAAGEKPKSREGSGGPOESSRDKRPL 180
Db      121 PATTARAGGPKAGSRGFRFAGHSEAGGSGDRRRAAGEKPKSREGSGGPOESSRDKRPL 180
Qy      181 SGPDVGTPOGAGIAGAKLAAGRPFTYPRADTDHPSRGAQGEPHDVAENGPAGGLAIP 240
Db      181 SGPDVGTPOGAGIAGAKLAAGRPFTYPRADTDHPSRGAQGEPHDVAENGPAGGLAIP 240
Qy      241 QSSSSSSRPPTARAGAPSPGVIGPHASEPQLAPPAAPVAPGPPGRSPQREPORVS 300
Db      241 QSSSSSSRPPTARAGAPSPGVIGPHASEPQLAPPAAPVAPGPPGRSPQREPORVS 300
Qy      241 QSSSSSSRPPTARAGAPSPGVIGPHASEPQLAPPAAPVAPGPPGRSPQREPORVS 300
Db      241 QSSSSSSRPPTARAGAPSPGVIGPHASEPQLAPPAAPVAPGPPGRSPQREPORVS 300
Qy      301 HEOFRALQLVDPGDPGRSYLNFITKIGSGTGVICIAVRSNGKLVAAKMDLRQQR 360
Db      301 HEOFRALQLVDPGDPGRSYLNFITKIGSGTGVICIAVRSNGKLVAAKMDLRQQR 360
Qy      361 ELLFNEVIMRDYOHENNVEMVNSYLVDLWVMEFLEGALTDIVTHRMNEEQIAAV 420
Db      361 ELLFNEVIMRDYOHENNVEMVNSYLVDLWVMEFLEGALTDIVTHRMNEEQIAAV 420
Qy      421 CLAVALQALSVLHAQGVYHDIKSDSITLTHDGRVKLSDFGCAQVSKEYVRRKSLVGTPE 480
Db      421 CLAVALQALSVLHAQGVYHDIKSDSITLTHDGRVKLSDFGCAQVSKEYVRRKSLVGTPE 480
Qy      481 WMAPELISRLPYGPEVDIWSLGIWVEMWDGEPYNEPPLKMKMIRDLNLPRLKNLHK 540
Db      481 WMAPELISRLPYGPEVDIWSLGIWVEMWDGEPYNEPPLKMKMIRDLNLPRLKNLHK 540
Qy      541 VSPSLKGFDRLLVDRDPAQRATAELKHPFLAKAGPPASIVPLMKQN 588
Db      541 VSPSLKGFDRLLVDRDPAQRATAELKHPFLAKAGPPASIVPLMKQN 588

RESULT 10
ADJ96654
ID ADJ96654 standard; protein; 593 AA.
XX
AC ADJ96654;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human sterile protein kinase STE20 Paks_m protein Segid 111.
XX
KW kinase; human; tyrosine protein kinase; serine/threonine protein kinase;
KM PKA; STK; gene therapy; cancer; immune-related disease;
KM cardiovascular disease; brain; neuronal associated disease; metabolic;
KM inflammatory disorder; cytostatic; neuroprotective; immunomodulator;
KM antiinflammatory; enzyme; sterile protein kinase STE20; Paks_m.

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XX Homo sapiens.  
 OS 59.  
 PN WO2004006938-A2.  
 PD 22-JAN-2004.  
 PF 15-JUL-2003; 2003WO-US021730.  
 PR 15-JUL-2002; 2002US-0395632P.  
 PA (SUGB-) SUGEN INC.  
 PI Whyte D, Manning G, Caenepeel S;  
 DR WPI: 2004-122753/12.  
 DR N-PSDB; ADJ96588.  
 XX New nucleic acid molecule encoding a kinase polypeptide, useful for  
 PT preparing a composition for treating diseases or disorders, e.g., cancer,  
 PT or neurological, immunological or inflammatory disorders.  
 PS Claim 1; SEQ ID NO 111; 366pp; English.  
 XX This invention relates to a novel isolated, enriched or purified nucleic  
 CC acid molecule that encodes a kinase polypeptide. Specifically, it relates  
 CC to human tyrosine and serine/threonine protein kinases (PTK's and STK's),  
 CC as well as protein kinase-like enzymes. The present invention describes  
 CC screening methods to identify agonists, antagonists and antibodies that  
 CC can be used to modulate the activity or function of the mammalian kinase  
 CC enzymes. As such, these compositions can be used for gene therapy  
 CC purposes to treat diseases or disorders including cancer, immune-related  
 CC diseases, cardiovascular disease, brain or neuronal associated disease,  
 CC metabolic and inflammatory disorders. Accordingly, they exhibit  
 CC cytostatic, neuroprotective, immunomodulator and antiinflammatory  
 CC activities. This polypeptide sequence is a human kinase protein sequence  
 CC of the invention.  
 SQ Sequence 593 AA;  
 Query Match 92.6%; Score 2860; DB 8; Length 593;  
 Best Local Similarity 92.6%; Pred. No. 1,5e-199;  
 Matches 550; Conservative 10; Mismatches 30; Indels 4; Gaps 2;  
 QY 1 MFGKKKRVETISAPSNFEHRVHTGPDHOKFTGLPRQMSLIESARRPKLVDPACT 60  
 DB 1 MFGKKKRVETISAPSNFEHRVHTGPDHOKFTGLPRQMSLIESARRPKLVDPACT 60  
 QY 61 SIQPGAKTIVGSKGAKDGLATLLDEFFENMSVTRSNLSLRDSEPPPARARQENGMPEE 120  
 DB 61 SIQPGAKTIVGSKGAKDGLATLLDEFFENMSVTRSNLSLRDSEPPPARARQENGMPEE 120  
 QY 121 PATTARGGCGKRGSKRFGAGSEBAGGSGDRRRAPBEKPKSSRGGSGPSSRDKRL 180  
 DB 121 PATTARGGCGKRGSKRFGAGSEBAGGSGDRRRAPBEKPKSSRGGSGPSSRDKRL 180  
 QY 121 RAAPARMAPDKGSSRARATGSHSEAGSGDRRRVGEKEPKSSRDGPGPOBASDKRPL 180  
 DB 121 RAAPARMAPDKGSSRARATGSHSEAGSGDRRRVGEKEPKSSRDGPGPOBASDKRPL 180  
 QY 181 SGPDVGTGPDPAAGSAGKLAAGRPFTYPRADTDHPSRGAQSEPHDVANGSAGSLAP 240  
 DB 181 SGPDVGTGPDPAAGSAGKLAAGRPFTYPRADTDHPSRGAQSEPHDVANGSAGSLAP 240  
 QY 241 QSSSSSSRPPTARAGAPSPGVLPAPASEPOLAPPA---CTPAAPAVPGPPGRRSPQREPO 297  
 DB 241 QSSSSSSRPPTARAGAPSPGVLPAPASEPOLAPPA---CTPAAPAVPGPPGRRSPQREPO 297  
 QY 241 QSSSSSSRPPTARAGAPSPGVLPAPASEPOLAPPA---CTPAAPAVPGPPGRRSPQREPO 299  
 DB 241 QSSSSSSRPPTARAGAPSPGVLPAPASEPOLAPPA---CTPAAPAVPGPPGRRSPQREPO 299  
 QY 298 RVSHQGFRAALQLVDPGPPRSYLVNFTIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQ 357  
 DB 298 RVSHQGFRAALQLVDPGPPRSYLVNFTIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQ 357  
 QY 300 RVSHQGFRAALQLVDPGPPRSYLVNFTIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQ 359  
 DB 300 RVSHQGFRAALQLVDPGPPRSYLVNFTIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQ 359  
 QY 358 QRRLLLENEVVMRDYOHENNVEMTNSYVGPDELWVWFELEGALTDIVTTRNNEBOI 417  
 DB 358 QRRLLLENEVVMRDYOHENNVEMTNSYVGPDELWVWFELEGALTDIVTTRNNEBOI 417  
 QY 360 QRRLLLENEVVMRDYOHENNVEMTNSYVGPDELWVWFELEGALTDIVTTRNNEBOI 419  
 DB 360 QRRLLLENEVVMRDYOHENNVEMTNSYVGPDELWVWFELEGALTDIVTTRNNEBOI 419

QY 418 AAVCLAVIALSALVLAHQGVIRHDIKSDSLTLTHDGRVXLSDFGCAQVSKVPRRKSIVG 477  
 DB 420 AAVCLAVIALSALVLAHQGVIRHDIKSDSLTLTHDGRVXLSDFGCAQVSKVPRRKSIVG 479  
 QY 478 TPYMAPELISRLPYGPEVDIWSLGIWYIEMVDGPPYFNNEPPLKAMKIRIINLPPRLKN 537  
 DB 480 TPYMAPELISRLPYGPEVDIWSLGIWYIEMVDGPPYFNNEPPLKAMKIRIINLPPRLKN 539  
 QY 538 LHKVPSLKGFLDRLLVDPAPQATAAELKHPFLAKGPPASIVPLMRQNRTR 591  
 DB 540 LHKVPSLKGFLDRLLVDPAPQATAAELKHPFLAKGPPASIVPLMRQNRTR 593  
 RESULT 11  
 ID ABM84642 standard; protein; 522 AA.  
 AC ABM84642;  
 XX 18-NOV-2004 (first entry)  
 DT Human diagnostic and therapeutic protein SEQ ID NO:4891.  
 DE gene therapy; human diagnostic and therapeutic polynucleotide; ditp.  
 XX Homo sapiens.  
 OS WO2004023973-A2.  
 PN 25-MAR-2004.  
 PD 12-SEP-2003; 2003WO-US028227.  
 PF 12-SEP-2002; 2002US-0410259P.  
 PR 12-SEP-2002; 2002US-0410260P.  
 XX (INCY-) INCYTE CORP.  
 PA Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
 PI Harshorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV;  
 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;  
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;  
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LJ;  
 PI Lagace RB, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kirton ES;  
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
 PI Patry S, Shi X, Suarez CJ;  
 XX WPI: 2004-329368/30.  
 DR N-PSDB; ACN43294.  
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
 PT in diagnosing a condition, disease or disorder associated with human  
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
 PT in gene mapping.  
 PS Claim 27; Page; 190pp; English.  
 XX The invention relates to novel diagnostic and therapeutic polynucleotides  
 CC selected from one of the 2722 sequences defined in the specification. A  
 CC polynucleotide of the invention may have a use in gene therapy. The human  
 CC diagnostic and therapeutic polynucleotides (ditp) or polypeptides may be  
 CC used to diagnose a particular condition, disease or disorder associated  
 CC with human molecules, e.g. cell proliferative disorders,  
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
 CC disorder, neurological disorders, gastrointestinal disorders, or  
 CC infections caused by virus, bacteria, fungi or parasite. The ditp  
 CC molecules may also be used in genetic mapping, in identifying individuals  
 CC from minute biological samples, in detecting single nucleotide  
 CC polymorphisms, as molecular weight markers, and for somatic or germ-line  
 CC gene therapy. The present sequence represents a ditp protein of the  
 CC invention. Note: The sequence data for this patent is not represented in  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)



XX Sequence 522 AA;  
 SQ  
 Query Match 86.6%; Score 2674.5; DB 8; Length 522;  
 Best Local Similarity 88.2%; Pred. No. 4.2e-186;  
 Matches 521; Conservative 0; Mismatches 1; Indels 69; Gaps 1;  
 1 MEGKRRKRVISAPSNFHRVHTGPDQHOEOKFTGLPRQMSLIESARPKPLVDPACT 60  
 1 MEGKRRKRVISAPSNFHRVHTGPDQHOEOKFTGLPRQMSLIESARPKPLVDPACT 60  
 1 MEGKRRKRVISAPSNFHRVHTGPDQHOEOKFTGLPRQMSLIESARPKPLVDPACT 60  
 61 SIOPGAPKTIIVGSGKAGDGLTLLDEFENNSVTRNSLRDPPPPARAOENGMPEE 120  
 61 SIOPGAPKTIIVGSGKAGDGLTLLDEFENNSVTRNSLRDPPPPARAOENGMPEE 120  
 121 PATYARGGPGKAGSRGRFAGHSEAGGSGDRRRAGEKPKSRBSGGGPOESSRDKPL 180  
 121 PATYARGGPGKAGSRGRFAGHSEAGGSGDRRRAGEKPKSRBSGGGPOESSRDKPL 180  
 121 PATYARGGPGKAGSRGRFAGHSEAGGSGDRRRAGEKPKSRBSGGGPOESSRDKPL 180  
 181 SGPVGTGPAGLASGAKLAAGRPENTYPRADTDHPSRGAQGEPPHDVAPNGPSAGGLATP 240  
 125 -----AKAKLAAGRPENTYPRADTDHPSRGAQGEPPHDVAPNGPSAGGLATP 171  
 241 QSSSSSRPPTARAGAPSPGVLPASBPOLAPACTPAAPAVPGPGRSPQREPORYS 300  
 172 QSSSSSRPPTARAGAPSPGVLPASBPOLAPACTPAAPAVPGPGRSPQREPORYS 231  
 301 HEOPRAALQLVDPGDPSPSYLDFIKIGSGTGICVIAVRSSGKLVAVKMDLRKQRR 360  
 233 HEOPRAALQLVDPGDPSPSYLDFIKIGSGTGICVIAVRSSGKLVAVKMDLRKQRR 291  
 361 ELLFNEVIMRDYQHENVNEMTNSYLVDGLVWVMELEGALTDIVTTRNNEEOIAV 420  
 292 ELLFNEVIMRDYQHENVNEMTNSYLVDGLVWVMELEGALTDIVTTRNNEEOIAV 351  
 421 CLAVLQALSVLAAGVIRHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKRSIVGTPT 480  
 352 CLAVLQALSVLAAGVIRHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKRSIVGTPT 411  
 481 WMAPELISRLPYGPEVDIVSLGIMVIEWDGEPPEYNEPPLKAMKIRDNLPRLKNLHK 540  
 412 WMAPELISRLPYGPEVDIVSLGIMVIEWDGEPPEYNEPPLKAMKIRDNLPRLKNLHK 471  
 541 VSPSLKGFRLDLVDPDAQRTAAELIKHPFLAKGPPASIVPLMKQNRTR 591  
 472 VSPSLKGFRLDLVDPDAQRTAAELIKHPFLAKGPPASIVPLMKQNRTR 522  
 Db  
 RESULT 12  
 ABM84644  
 ID ABM84644 standard; protein; 522 AA.  
 AC ABM84644;  
 DT 18-NOV-2004 (first entry)  
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4893.  
 KM gene therapy; human diagnostic and therapeutic polynucleotide; dthp.  
 OS Homo sapiens.  
 XX WO2004023973-A2.  
 XX PN 25-MAR-2004.  
 XX PD 12-SEP-2003; 2003WO-US028227.  
 XX PF 12-SEP-2002; 2002US-0410259P.  
 XX PR 12-SEP-2002; 2002US-0410260P.  
 XX PA (INCY-) INCYTE CORP.  
 XX

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,  
 PI Harthorne TA, Suchorski MT, Altus CM, Plets SJ, Rider LV,  
 PI Mooney EM, Deleage AM, Pansar IS, Banville SC, Reddy TP,  
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH,  
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL,  
 PI Lagace RB, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitron ES,  
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,  
 PI Patuty S, Shi X, Share CJ,  
 DR WPI, 2004-329368/30.  
 DR N-PSDB; ACN43296.  
 XX  
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
 PT in diagnosing a condition, disease or disorder associated with human  
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
 PT in gene mapping.  
 XX  
 XX Claim 27; Page; 190pp; English.  
 PS  
 XX  
 CC The invention relates to novel diagnostic and therapeutic polynucleotides  
 CC selected from one of the 2722 sequences defined in the specification. A  
 CC polynucleotide of the invention may have a use in gene therapy. The human  
 CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be  
 CC used to diagnose a particular condition, disease or disorder associated  
 CC with human molecules, e.g. cell proliferative disorders,  
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
 CC disorder, neurological disorders, gastrointestinal disorders, or  
 CC infections caused by virus, bacteria, fungi or parasite. The dthp  
 CC molecules may also be used in genetic mapping, in identifying individuals  
 CC from minute biological samples, in detecting single nucleotide  
 CC polymorphisms, as molecular weight markers, and for somatic or germ-line  
 CC gene therapy. The present sequence represents a dthp protein of the  
 CC invention. Note: The sequence data for this patent is not represented in  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at [www.wipo.int/pct/en/sequences/11sting.htm](http://www.wipo.int/pct/en/sequences/11sting.htm)  
 CC  
 SQ Sequence 522 AA;  
 Query Match 86.6%; Score 2674.5; DB 8; Length 522;  
 Best Local Similarity 88.2%; Pred. No. 4.2e-186;  
 Matches 521; Conservative 0; Mismatches 1; Indels 69; Gaps 1;  
 1 MEGKRRKRVISAPSNFHRVHTGPDQHOEOKFTGLPRQMSLIESARPKPLVDPACT 60  
 1 MEGKRRKRVISAPSNFHRVHTGPDQHOEOKFTGLPRQMSLIESARPKPLVDPACT 60  
 1 MEGKRRKRVISAPSNFHRVHTGPDQHOEOKFTGLPRQMSLIESARPKPLVDPACT 60  
 61 SIOPGAPKTIIVGSGKAGDGLTLLDEFENNSVTRNSLRDPPPPARAOENGMPEE 120  
 61 SIOPGAPKTIIVGSGKAGDGLTLLDEFENNSVTRNSLRDPPPPARAOENGMPEE 120  
 121 PATYARGGPGKAGSRGRFAGHSEAGGSGDRRRAGEKPKSRBSGGGPOESSRDKPL 180  
 121 PATYARGGPGKAGSRGRFAGHSEAGGSGDRRRAGEKPKSRBSGGGPOESSRDKPL 180  
 121 PATYARGGPGKAGSRGRFAGHSEAGGSGDRRRAGEKPKSRBSGGGPOESSRDKPL 180  
 181 SGPVGTGPAGLASGAKLAAGRPENTYPRADTDHPSRGAQGEPPHDVAPNGPSAGGLATP 240  
 125 -----AKAKLAAGRPENTYPRADTDHPSRGAQGEPPHDVAPNGPSAGGLATP 171  
 241 QSSSSSRPPTARAGAPSPGVLPASBPOLAPACTPAAPAVPGPGRSPQREPORYS 300  
 172 QSSSSSRPPTARAGAPSPGVLPASBPOLAPACTPAAPAVPGPGRSPQREPORYS 231  
 301 HEOPRAALQLVDPGDPSPSYLDFIKIGSGTGICVIAVRSSGKLVAVKMDLRKQRR 360  
 233 HEOPRAALQLVDPGDPSPSYLDFIKIGSGTGICVIAVRSSGKLVAVKMDLRKQRR 291  
 361 ELLFNEVIMRDYQHENVNEMTNSYLVDGLVWVMELEGALTDIVTTRNNEEOIAV 420  
 292 ELLFNEVIMRDYQHENVNEMTNSYLVDGLVWVMELEGALTDIVTTRNNEEOIAV 351  
 421 CLAVLQALSVLAAGVIRHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKRSIVGTPT 480  
 352 CLAVLQALSVLAAGVIRHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKRSIVGTPT 411  
 Db

QY 481 WMAPELISRLPYGPEVDIWSLGIWVLEMDGPPYFNBPPLKAMKIMRDNLPRLKNLHK 540  
 Db 412 WMAPELISRLPYGPEVDIWSLGIWVLEMDGPPYFNBPPLKAMKIMRDNLPRLKNLHK 471  
 QY 541 VSPSLKGFLLRLVDPQATATAEELKHPLAKAGPPASIVPLMRQNRTR 591  
 Db 472 VSPSLKGFLLRLVDPQATATAEELKHPLAKAGPPASIVPLMRQNRTR 522

RESULT 13  
 AEM84645  
 ID AEM84645 standard; protein; 522 AA.  
 XX AEM84645;  
 AC AEM84645;  
 DT 18-NOV-2004 (first entry)  
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4894.  
 XX  
 KM gene therapy; human diagnostic and therapeutic polynucleotide; dittp.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004023973-A2.  
 XX  
 PD 25-MAR-2004.  
 XX  
 PF 12-SEP-2003; 2003WO-US028227.  
 XX  
 PR 12-SEP-2002; 2002US-0410259P.  
 PR 12-SEP-2002; 2002US-0410260P.  
 XX  
 XX  
 PA (INCY-) INCYTE CORP.  
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,  
 PI Harshborne RA, Suchorolski MT, Altus CM, Plets SJ, Elder LV,  
 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;  
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH,  
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL,  
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Valt UA, Kliton ES,  
 PI Xu Y, Kwong M, Policky JT, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
 PI Patuty S, Shi X, Suarez CJ;  
 XX  
 DR MPI: 2004-329368/30.  
 DR N-PSDB; ACN43297.  
 XX  
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful  
 PT in diagnosing a condition, disease or disorder associated with human  
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
 PT in gene mapping.  
 XX  
 PS Claim 27; Page; 190pp; English.  
 XX  
 CC The invention relates to novel diagnostic and therapeutic polynucleotides  
 CC selected from one of the 2722 sequences defined in the specification. A  
 CC polynucleotide of the invention may have a use in gene therapy. The human  
 CC diagnostic and therapeutic polynucleotides (dittp) or polypeptides may be  
 CC used to diagnose a particular condition, disease or disorder associated  
 CC with human molecules, e.g. cell proliferative disorders,  
 CC autoimmune/inflammatory disorder, developmental disorders,  
 CC infections caused by virus, bacteria, fungi or parasite. The dittp  
 CC molecules may also be used in genetic mapping, in identifying individuals  
 CC from minute biological samples, in detecting single nucleotide  
 CC polymorphisms, as molecular weight markers, and for somatic or germline  
 CC gene therapy. The present sequence represents a dittp protein of the  
 CC invention. Note: The sequence data for this patent is not represented in  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm  
 CC  
 XX Sequence 522 AA;  
 SQ

Query Match 86.6%; Score 2674.5; DB 8; Length 522;  
 Best Local Similarity 88.2%; Pred. No. 4.2e-186;  
 Matches 521; Conservative 0; Mismatches 1; Indels 69; Gaps 1;

QY 1 MFGKKRKEVEISAPNPFHRVHTGPDQHEOKFTGLPRWQOSLIESSARRKPLVDPACIT 60  
 Db 1 MFGKKRKEVEISAPNPFHRVHTGPDQHEOKFTGLPRWQOSLIESSARRKPLVDPACIT 60  
 QY 61 STOPGAPRTIVRSGKAGDQALTLTLDDEFNNVYRNSLRDPSPPARRAQENGMBEE 120  
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 QY 121 PATTARGGPKAGSGRGRFAGHSEAGSGSDRRRAGPEKRRPKSSRBGSGQPOESSRDKRPL 180  
 Db 121 PATTARGGPKAGSGRGRFAGHSEAGSGSDRRRAGPEKRRPKSSRBGSGQPOESSRDKRPL 180  
 QY 181 SGPDVGTPOAGLASGATLAAGRPPNTYPRADTDHPSGAGCEPHDVA PNGSAGGLAIP 240  
 Db 181 SGPDVGTPOAGLASGATLAAGRPPNTYPRADTDHPSGAGCEPHDVA PNGSAGGLAIP 240  
 QY 125 -----AAGATLAAGRPPNTYPRADTDHPSGAGCEPHDVA PNGSAGGLAIP 171  
 Db 125 -----AAGATLAAGRPPNTYPRADTDHPSGAGCEPHDVA PNGSAGGLAIP 171  
 QY 241 OSSSSSRPPTRRARGAPSGVLYGPHASRPOLAPACTPAAPVAPGPPGRSPQREPORVS 300  
 Db 241 OSSSSSRPPTRRARGAPSGVLYGPHASRPOLAPACTPAAPVAPGPPGRSPQREPORVS 300  
 QY 172 OSSSSSRPPTRRARGAPSGVLYGPHASRPOLAPACTPAAPVAPGPPGRSPQREPORVS 231  
 Db 172 OSSSSSRPPTRRARGAPSGVLYGPHASRPOLAPACTPAAPVAPGPPGRSPQREPORVS 231  
 QY 301 HEQFRAALQLVDPGDPSPSYLDNFIKIGEGSTGIVCIATVRSAGLVAVKMDLKKQQR 360  
 Db 301 HEQFRAALQLVDPGDPSPSYLDNFIKIGEGSTGIVCIATVRSAGLVAVKMDLKKQQR 360  
 QY 232 HEQFRAALQLVDPGDPSPSYLDNFIKIGEGSTGIVCIATVRSAGLVAVKMDLKKQQR 291  
 Db 232 HEQFRAALQLVDPGDPSPSYLDNFIKIGEGSTGIVCIATVRSAGLVAVKMDLKKQQR 291  
 QY 361 ELLFNEVVIWRDYQHENYVENYNSYLVDDELWVMEFLEGALTDIVHTRNNEQIAAV 420  
 Db 361 ELLFNEVVIWRDYQHENYVENYNSYLVDDELWVMEFLEGALTDIVHTRNNEQIAAV 420  
 QY 232 ELLFNEVVIWRDYQHENYVENYNSYLVDDELWVMEFLEGALTDIVHTRNNEQIAAV 351  
 Db 232 ELLFNEVVIWRDYQHENYVENYNSYLVDDELWVMEFLEGALTDIVHTRNNEQIAAV 351  
 QY 421 CLAVALQALSYLAQGVHHRDIKSDSILLTHDGRVLYSPFGCAQYSKEVPRKSLVGTPT 480  
 Db 421 CLAVALQALSYLAQGVHHRDIKSDSILLTHDGRVLYSPFGCAQYSKEVPRKSLVGTPT 480  
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 QY 541 VSPSLKGFLLRLVDPQATATAEELKHPLAKAGPPASIVPLMRQNRTR 591  
 Db 541 VSPSLKGFLLRLVDPQATATAEELKHPLAKAGPPASIVPLMRQNRTR 522  
 QY 472 VSPSLKGFLLRLVDPQATATAEELKHPLAKAGPPASIVPLMRQNRTR 522  
 Db 472 VSPSLKGFLLRLVDPQATATAEELKHPLAKAGPPASIVPLMRQNRTR 522

RESULT 14  
 AEM84648  
 ID AEM84648 standard; protein; 517 AA.  
 XX  
 AC AEM84648;  
 XX  
 DT 18-NOV-2004 (first entry)  
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4897.  
 XX  
 KM gene therapy; human diagnostic and therapeutic polynucleotide; dittp.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004023973-A2.  
 XX  
 PD 25-MAR-2004.  
 XX  
 PF 12-SEP-2003; 2003WO-US028227.  
 XX  
 PR 12-SEP-2002; 2002US-0410259P.  
 PR 12-SEP-2002; 2002US-0410260P.  
 XX  
 XX  
 PA (INCY-) INCYTE CORP.  
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,  
 PI Harshborne RA, Suchorolski MT, Altus CM, Plets SJ, Elder LV,  
 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;  
 XX

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Geregin EH;  
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL;  
 PI Lagae RE, Spiro PA, Stewart EA, Wingrove J, Viltz UA, Kitron ES;  
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
 PI Patuty S, Shi X, Suarez CJ;  
 DR MPI: 2004-329368/30.  
 DR N-PSDB; ACN43300.  
 XX  
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful  
 PT in diagnosing a condition, disease or disorder associated with human  
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
 PT in gene mapping.  
 XX  
 XX Claim 27; Page: 190pp; English.  
 CC The invention relates to novel diagnostic and therapeutic polynucleotides  
 CC selected from one of the 2722 sequences defined in the specification. A  
 CC polynucleotide of the invention may have a use in gene therapy. The human  
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
 CC used to diagnose a particular condition, disease or disorder associated  
 CC with human molecules, e.g. cell proliferative disorders,  
 CC autoimmune/inflammatory disorder, developmental disorders,  
 CC infection, neurological disorders, gastrointestinal disorders, endocrine  
 CC infections caused by virus, bacteria, fungi or parasite. The dithp  
 CC molecules may also be used in genetic mapping, in identifying individuals  
 CC from minute biological samples, in detecting single nucleotide  
 CC polymorphisms, as molecular weight markers, and for somatic or germline  
 CC gene therapy. The present sequence represents a dithp protein of the  
 CC invention. Note: The sequence data for this patent is not represented in  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
 CC  
 XX  
 XX Sequence 517 AA;

Query Match 86.1%; Score 2662; DB 8; Length 517;  
 Best Local Similarity 87.3%; Pred. No. 3, 4e-185;  
 Matches 516; Conservative 0; Mismatches 1; Indels 74; Gaps 1;

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 DB 1 MFGKRRKRVISAPSNFEHRVHTGFDQHQKFTGLPRQMSLIESARRPKPLVDACIT 60  
 QY 61 STQPGAKTIVVSGSKAKGALTLLDEFENMSVTNSNLRDPPPPARAQENEMPE 120  
 DB 61 STQPGAKTIVVSGSKAKGALTLLDEFENMSVTNSNLRDPPPPARAQENEMPE 120  
 QY 121 PATTARAGPGKAGSRGFRGSHSAGGSGDRRAAGPEKPKSRRSGSGGPOESSRDKRPL 180  
 DB 121 PATTARAGPGKAGSRGFRGSHSAGGSGDRRAAGPEKPKSRRSGSGGPOESSRDKRPL 180  
 QY 181 SGPDVGTPOPGAGLASCAGLAPFNTYPRADTHPSRGAGOEPRHDVANGSPAGLAI 240  
 DB 181 SGPDVGTPOPGAGLASCAGLAPFNTYPRADTHPSRGAGOEPRHDVANGSPAGLAI 240  
 QY 241 QSSSSSSRPTTRAKAPSPGVAGPHASEPOLAPACTPAAPVPGPPGPPRPPRPPRPPR 300  
 DB 241 QSSSSSSRPTTRAKAPSPGVAGPHASEPOLAPACTPAAPVPGPPGPPRPPRPPRPPR 300  
 QY 301 HSGFRALGLVDPGPRSYLDNFIRIGSGSTGIVICATVRSRSGKVAVAKMDLRQQR 360  
 DB 301 HSGFRALGLVDPGPRSYLDNFIRIGSGSTGIVICATVRSRSGKVAVAKMDLRQQR 360  
 QY 361 ELLFNEVIMRDYOHENVMNTSYLVGDELWVMEFLBGALTDIVTHRNNEOIAAV 420  
 DB 361 ELLFNEVIMRDYOHENVMNTSYLVGDELWVMEFLBGALTDIVTHRNNEOIAAV 420  
 QY 421 CLAVALALSVLAHAGVYIHRDSDSLILTHDGRVKSDFGFCQVSKVPRKSLVGT 480  
 DB 421 CLAVALALSVLAHAGVYIHRDSDSLILTHDGRVKSDFGFCQVSKVPRKSLVGT 480  
 QY 481 WMAPELISRLPYGPEVDIWSLIGIMVTEMVDEGPPYENEPPLKMKKIRIINLPRILNKLK 540  
 DB 481 WMAPELISRLPYGPEVDIWSLIGIMVTEMVDEGPPYENEPPLKMKKIRIINLPRILNKLK 540

DB 407 WMAPELISRLPYGPEVDIWSLIGIMVTEMVDEGPPYENEPPLKMKKIRIINLPRILNKLK 466  
 QY 541 VSPSLKGFLLDLNDDPAORATRAAEILKHPFLAKGPPASITPLMRONTR 591  
 DB 467 VSPSLKGFLLDLNDDPAORATRAAEILKHPFLAKGPPASITPLMRONTR 517

## RESULT 15

ID ABM84647 standard; protein; 517 AA.

AC ABM84647;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pprotein SEQ ID NO:4896.

KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

OS Homo sapiens.

PN WO2004023973-A2.

PD 25-MAR-2004.

PF 12-SEP-2003; 2003WO-US028227.

PR 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

PI Hartschorne TA, Suchorolski MT, Altus CM, Plets SJ, Sider LV;

PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Geregin EH;

PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL;

PI Lagae RE, Spiro PA, Stewart EA, Wingrove J, Viltz UA, Kitron ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

PI Patuty S, Shi X, Suarez CJ;

PS Claim 27; Page: 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides

XX selected from one of the 2722 sequences defined in the specification. A

XX polynucleotide of the invention may have a use in gene therapy. The human

XX diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be

XX used to diagnose a particular condition, disease or disorder associated

XX with human molecules, e.g. cell proliferative disorders,

XX autoimmune/inflammatory disorder, developmental disorder, endocrine

XX infection, neurological disorders, gastrointestinal disorders, or

XX infections caused by virus, bacteria, fungi or parasite. The dithp

XX molecules may also be used in genetic mapping, in identifying individuals

XX from minute biological samples, in detecting single nucleotide

XX polymorphisms, as molecular weight markers, and for somatic or germline

XX gene therapy. The present sequence represents a dithp protein of the

XX invention. Note: The sequence data for this patent is not represented in

XX the printed specification, but was obtained in electronic format directly

XX from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

XX  
 XX Sequence 517 AA;

Query Match 86.1%; Score 2662; DB 8; Length 517;  
 Best Local Similarity 87.3%; Pred. No. 3, 4e-185;  
 Matches 516; Conservative 0; Mismatches 1; Indels 74; Gaps 1;

QY 1 MFGRRKKRVHISAPSNFHRVHTGFDQHEQKFTGLPRWQSLIESARRPKPLVDPACT 60  
Db 1 MFGRRKKRVHISAPSNFHRVHTGFDQHEQKFTGLPRWQSLIESARRPKPLVDPACT 60  
QY 61 SIOPGAPKTIYRSGSKAGKOGALTLILDEFENMSVTRNSLNRDSDPPPPARARQENGMPBE 120  
Db 61 SIOPGAPKTIYRSGSKAGKOGALTLILDEFENMSVTRNSLNRDSDPPPPARARQENGMPBE 120  
QY 121 PATTAGGPGKAGSRFRFAGHSEAGGSGDRRRAGBEKPKSSREGSGGPOESSRDKRPL 180  
Db 121 PATTAGGPGKAGSRFRFAGHSEAGGSGDRRRAGBEKPKSSREGSGGPOESSRDKRPL 180  
QY 181 SGPDVGTPOPAGIAGAKLAAGRPNTYPRADTDHPSRGAQGEPRDVA PNGPSAGLAIP 240  
Db 181 SGPDVGTPOPAGIAGAKLAAGRPNTYPRADTDHPSRGAQGEPRDVA PNGPSAGLAIP 240  
QY 241 QSSSSSSRPPTARAGAPSPGYLGPHASEPOLAPPACTPAPAPVPGPPGPRSPOREPORVS 300  
Db 241 QSSSSSSRPPTARAGAPSPGYLGPHASEPOLAPPACTPAPAPVPGPPGPRSPOREPORVS 300  
QY 301 HEQFRAALQLVYDPGDPBSYLDNFKITIGEGSTGIVCIATVRS SGLVA VKMDLRKQORR 360  
Db 301 HEQFRAALQLVYDPGDPBSYLDNFKITIGEGSTGIVCIATVRS SGLVA VKMDLRKQORR 360  
QY 361 ELLENEVVIMRDYOHENNVEMYNSTYVGDELMVMEFLGGALTDIVTTRANEQIAY 420  
Db 361 ELLENEVVIMRDYOHENNVEMYNSTYVGDELMVMEFLGGALTDIVTTRANEQIAY 420  
QY 421 CLAVLQALSVLAHQVITHRODKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSIVGTPY 480  
Db 381 -----XLSDFGFCQVSKVPRRKSIVGTPY 406  
QY 481 WMADELISRLEPYGEVDIWSLGIWIVEMVDEPPYENBPLKAMKMI RDNLPPRLKNLHK 540  
Db 407 WMADELISRLEPYGEVDIWSLGIWIVEMVDEPPYENBPLKAMKMI RDNLPPRLKNLHK 466  
QY 541 VSPSLKGFILRLIVRDPARATAAEILKHPFLAKAGPPASIVPLMRQNRTR 591  
Db 467 VSPSLKGFILRLIVRDPARATAAEILKHPFLAKAGPPASIVPLMRQNRTR 517

Search completed: March 15, 2005, 11:26:30  
Job time : 207.374 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 15, 2005, 11:30:37 ; Search time 160.787 Seconds  
(without alignments)  
1212.403 Million cell updates/sec

Title: US-10-693-367-2

Perfect score: 3090

Sequence: 1 MFGKRRKRVETISAPNFHR.....LAKAGPPASIVPMRQNR 591

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:  
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20: /cgn2\_6/prodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	3090	100.0	591	14	US-10-134-102-4
3	3090	100.0	591	15	US-10-394-322A-48
4	3090	100.0	591	15	US-10-693-367-2
5	3090	100.0	591	17	US-10-893-025-5
6	3075	99.5	588	14	US-10-134-102-1
7	2860	92.6	593	16	US-10-618-941-111
8	2860	92.6	593	16	US-09-291-417-30
9	1748	56.6	719	14	US-10-331-095-2
10	1731	56.0	719	14	US-10-331-095-2
11	1731	56.0	719	14	US-10-394-322A-49
12	1502	48.6	292	15	US-10-406-676-5
13	1502	48.6	292	15	US-10-406-676-5

14	1502	48.6	292	15	US-10-406-676-8	Sequence 8, Appl1
15	1502	48.6	292	15	US-10-406-676-9	Sequence 9, Appl1
16	1502	48.6	292	15	US-10-406-676-10	Sequence 10, Appl1
17	1502	48.6	292	15	US-10-406-676-11	Sequence 11, Appl1
18	1502	48.6	293	15	US-10-406-676-4	Sequence 4, Appl1
19	1497.5	48.5	639	14	US-10-134-102-6	Sequence 6, Appl1
20	1494.5	48.4	635	14	US-10-134-102-2	Sequence 2, Appl1
21	1481	47.9	292	15	US-10-406-676-7	Sequence 7, Appl1
22	1481	47.9	292	15	US-10-406-676-12	Sequence 12, Appl1
23	1473.5	47.7	681	10	US-09-291-417-29	Sequence 29, Appl1
24	1470.5	47.6	681	10	US-09-765-815-2	Sequence 2, Appl1
25	1421	46.0	292	15	US-10-406-676-15	Sequence 15, Appl1
26	1335.5	43.2	641	15	US-10-311-034-15	Sequence 15, Appl1
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28	1289	41.7	290	15	US-10-406-676-14	Sequence 13, Appl1
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30	1289	41.7	290	15	US-10-406-676-17	Sequence 17, Appl1
31	1277	41.3	290	15	US-10-693-367-3	Sequence 3, Appl1
32	1213	39.3	290	15	US-10-406-676-18	Sequence 18, Appl1
33	1209	39.1	290	15	US-10-406-676-19	Sequence 19, Appl1
34	1209	39.1	290	15	US-10-406-676-20	Sequence 20, Appl1
35	1147	37.1	292	15	US-10-406-676-21	Sequence 21, Appl1
36	1096.5	35.5	540	15	US-10-369-493-6482	Sequence 6482, Ap
37	1090.5	35.3	542	15	US-10-369-493-6483	Sequence 6483, Ap
38	1024.5	33.2	580	15	US-10-108-260A-3288	Sequence 3288, Ap
39	937.5	30.3	704	15	US-10-267-502-378	Sequence 378, App
40	924	29.9	544	15	US-10-267-502-382	Sequence 382, App
41	909	29.4	544	9	US-09-967-624-6	Sequence 6, Appl1
42	909	29.4	544	14	US-10-289-161A-6	Sequence 6, Appl1
43	909	29.4	544	15	US-10-394-322A-47	Sequence 47, Appl1
44	909	29.4	544	15	US-10-267-502-379	Sequence 379, App
45	909	29.4	544	16	US-10-757-262-36	Sequence 36, Appl1

#### ALIGNMENTS

RESULT 1	
US-09-291-417-103	
Sequence 103, Application US/09291417A	
Publication No. US20030050230A1	
GENERAL INFORMATION:	
APPLICANT: PLOWMAN, GREGORY	
APPLICANT: MARTINEZ, RICARDO	
APPLICANT: WHITE, DAVID	
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES	
FILE REFERENCE: 240/300	
CURRENT APPLICATION NUMBER: US/09/291,417A	
CURRENT FILING DATE: 1999-04-13	
EARLIER APPLICATION NUMBER: US 60/081,784	
EARLIER FILING DATE: 1998-04-14	
NUMBER OF SEQ ID NOS: 147	
SOFTWARE: FastSeq for Windows Version 3.0	
SEQ ID NO 103	
LENGTH: 591	
TYPE: PRT	
ORGANISM: Full Length Mammalian (Human) PAK5hu	
US-09-291-417-103	
Query Match	
Best Local Similarity 100.0%; Score 3090; DB 10; Length 591;	
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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DB	1 MFGKRRKRVETISAPNFHRVHTGPDQHEQKFTGLPRWQSLIESSARRPKPLVDPACTT 60
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DB	61 STOPGPKTIVGSKAKDGLTLIDFERMNSVYRNSLRDSDPPPARQENGMPE 120
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Db 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRAPEKPKRSREGSGGQESSRDKRL 180  
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Db 181 SGPDVGTPOPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240  
QY 241 QSSSSSRPPTARAGAPSPGVLPHASSEPOLAPACTPAAPVPGPGRSPQREPORVS 300  
Db 241 QSSSSSRPPTARAGAPSPGVLPHASSEPOLAPACTPAAPVPGPGRSPQREPORVS 300  
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Db 301 HEQFRAALQLVDPDPRSILDNFIKIGEGSTGICATVRSRSGKLVAVKMDLKKQQR 360  
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Db 361 ELLENFVIMRDOHENNVEMNSYLVDDELVMVMEFLGALTDIVTTRNNEEQIAAV 420  
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Db 421 CLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVLSDFGCAQVSKVPRKSLVGTPI 480  
QY 481 WMAPELISRLPYGPEVDIWSLIGIMVTEMVDEBPYPFNEPPLKAMKIRDNLPRLKNLHK 540  
Db 481 WMAPELISRLPYGPEVDIWSLIGIMVTEMVDEBPYPFNEPPLKAMKIRDNLPRLKNLHK 540  
QY 541 VSPSLKGFLLDRLLVDPDPAQRATAELKHPFLAKAGPPASIVPLMKQNRTR 591  
Db 541 VSPSLKGFLLDRLLVDPDPAQRATAELKHPFLAKAGPPASIVPLMKQNRTR 591

RESULT 2  
US-10-134-102-4  
; Sequence 4, Application US/10134102  
; Publication No. US20030186254A1  
; GENERAL INFORMATION:  
; APPLICANT: Weinick, Michael B.  
; APPLICANT: Moritz, Albrecht  
; APPLICANT: Comb, Michael J.  
; TITLE OF INVENTION: Regulation of HIV-Tat and Nef by the Pak4 kinase and its  
; FILE REFERENCE: CST-176 CIP  
; CURRENT APPLICATION NUMBER: US/10/134,102  
; PRIOR FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: 09/750,457  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: 60/173,939  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-134-102-4

Query Match 100.0%; Score 3090; DB 14; Length 591;  
Best Local Similarity 100.0%; Pred. No. 5,7e-161;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFGKRRKVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIESARRPKPLVDPACT 60  
Db 1 MFGKRRKVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIESARRPKPLVDPACT 60  
QY 61 SIOPGAPRTIVRSGKAGDGLTLLDDEFEMSVTRNSLRRDSPPPARARQENGMEE 120  
Db 61 SIOPGAPRTIVRSGKAGDGLTLLDDEFEMSVTRNSLRRDSPPPARARQENGMEE 120  
QY 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRAPEKPKRSREGSGGQESSRDKRL 180  
Db 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRAPEKPKRSREGSGGQESSRDKRL 180  
QY 181 SGPDVGTPOPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240

Db 181 SGPDVGTPOPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240  
QY 241 QSSSSSRPPTARAGAPSPGVLPHASSEPOLAPACTPAAPVPGPGRSPQREPORVS 300  
Db 241 QSSSSSRPPTARAGAPSPGVLPHASSEPOLAPACTPAAPVPGPGRSPQREPORVS 300  
QY 301 HEQFRAALQLVDPDPRSILDNFIKIGEGSTGICATVRSRSGKLVAVKMDLKKQQR 360  
Db 301 HEQFRAALQLVDPDPRSILDNFIKIGEGSTGICATVRSRSGKLVAVKMDLKKQQR 360  
QY 361 ELLENFVIMRDOHENNVEMNSYLVDDELVMVMEFLGALTDIVTTRNNEEQIAAV 420  
Db 361 ELLENFVIMRDOHENNVEMNSYLVDDELVMVMEFLGALTDIVTTRNNEEQIAAV 420  
QY 421 CLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVLSDFGCAQVSKVPRKSLVGTPI 480  
Db 421 CLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVLSDFGCAQVSKVPRKSLVGTPI 480  
QY 481 WMAPELISRLPYGPEVDIWSLIGIMVTEMVDEBPYPFNEPPLKAMKIRDNLPRLKNLHK 540  
Db 481 WMAPELISRLPYGPEVDIWSLIGIMVTEMVDEBPYPFNEPPLKAMKIRDNLPRLKNLHK 540  
QY 541 VSPSLKGFLLDRLLVDPDPAQRATAELKHPFLAKAGPPASIVPLMKQNRTR 591  
Db 541 VSPSLKGFLLDRLLVDPDPAQRATAELKHPFLAKAGPPASIVPLMKQNRTR 591

RESULT 3  
US-10-394-322A-48  
; Sequence 48, Application US/10394322A  
; Publication No. US2003023291A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.  
; APPLICANT: Prescott, John C.  
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS  
; FILE REFERENCE: 39750-0006 US  
; CURRENT APPLICATION NUMBER: US/10/394,322A  
; PRIOR FILING DATE: 2003-03-20  
; PRIOR APPLICATION NUMBER: US 60/366,892  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 48  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-394-322A-48

Query Match 100.0%; Score 3090; DB 15; Length 591;  
Best Local Similarity 100.0%; Pred. No. 5,7e-161;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFGKRRKVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIESARRPKPLVDPACT 60  
Db 1 MFGKRRKVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIESARRPKPLVDPACT 60  
QY 61 SIOPGAPRTIVRSGKAGDGLTLLDDEFEMSVTRNSLRRDSPPPARARQENGMEE 120  
Db 61 SIOPGAPRTIVRSGKAGDGLTLLDDEFEMSVTRNSLRRDSPPPARARQENGMEE 120  
QY 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRAPEKPKRSREGSGGQESSRDKRL 180  
Db 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRAPEKPKRSREGSGGQESSRDKRL 180  
QY 181 SGPDVGTPOPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240  
Db 181 SGPDVGTPOPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240  
QY 241 QSSSSSRPPTARAGAPSPGVLPHASSEPOLAPACTPAAPVPGPGRSPQREPORVS 300  
Db 241 QSSSSSRPPTARAGAPSPGVLPHASSEPOLAPACTPAAPVPGPGRSPQREPORVS 300

QY 301 HEOFRALQLVVDGPGPRSYLDFIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQRR 360  
DB 301 HEOFRALQLVVDGPGPRSYLDFIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQRR 360  
QY 361 ELLFNEVIMRDYQHENVEMVNSYLVGDELWVMEFLEGALTDIVTHRNMEQIAAV 420  
DB 361 ELLFNEVIMRDYQHENVEMVNSYLVGDELWVMEFLEGALTDIVTHRNMEQIAAV 420  
QY 421 CLAVALSVLAQVYIHRDIDKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKSLVGTPT 480  
DB 421 CLAVALSVLAQVYIHRDIDKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKSLVGTPT 480  
QY 481 WMAPELISRLPYGPEVDIWSLIGIMVEMVDGEPYPFNEPPLKAMKIRIIDLPPRLKNLHK 540  
DB 481 WMAPELISRLPYGPEVDIWSLIGIMVEMVDGEPYPFNEPPLKAMKIRIIDLPPRLKNLHK 540  
QY 541 VSPSLKGFIDRLVLRDPAQRATPAELIKHPFLAKAGPPASIVPLMRQNRTR 591  
DB 541 VSPSLKGFIDRLVLRDPAQRATPAELIKHPFLAKAGPPASIVPLMRQNRTR 591

## RESULT 4

US-10-693-367-2  
; Sequence 2, Application US/10693367  
; Publication No. US20040091992A1  
; GENERAL INFORMATION:  
; APPLICANT: The Trustees of Columbia University  
; APPLICANT: Manden, Audrey  
; TITLE OF INVENTION: PAK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE  
; FILE REFERENCE: 575/55311-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/10/693,367  
; CURRENT FILING DATE: 2003-10-24  
; PRIOR APPLICATION NUMBER: US/09/718,032  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: PCT/US99/11341  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 09/082,737  
; PRIOR FILING DATE: 1998-05-21  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: human  
US-10-693-367-2

Query Match 100.0%; Score 3090; DB 15; Length 591;  
Best Local Similarity 100.0%; Pred. No. 5.7e-161;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFGKRRKRVETISAPSNFHRVHTGPDQEQKFTGLPRQWQSLIEESARRPKPLVDPACIT 60  
DB 1 MFGKRRKRVETISAPSNFHRVHTGPDQEQKFTGLPRQWQSLIEESARRPKPLVDPACIT 60  
QY 61 STOPGAPKTIIVRSKAKGKAGLTLILDEFENMVSITNSLRDSDPPPPARAQENGMPEE 120  
DB 61 STOPGAPKTIIVRSKAKGKAGLTLILDEFENMVSITNSLRDSDPPPPARAQENGMPEE 120  
QY 121 PATTAGGPGKAGSRGRFAGHSEAGGSGDRRRAGPEKPKSRREGSGGPOESSRDKRPL 180  
DB 121 PATTAGGPGKAGSRGRFAGHSEAGGSGDRRRAGPEKPKSRREGSGGPOESSRDKRPL 180  
QY 181 SGPDVGTPOAGIAGAKLAAGRPFTTYPRADTDHPSRGAQGEPHDVAVNGPSAGGLAIP 240  
DB 181 SGPDVGTPOAGIAGAKLAAGRPFTTYPRADTDHPSRGAQGEPHDVAVNGPSAGGLAIP 240  
QY 241 QSSSSSSRPPTARAGAPSPGVLGPHASEPQLAPACTPAAPVPGPGPRSPQREPORVS 300  
DB 241 QSSSSSSRPPTARAGAPSPGVLGPHASEPQLAPACTPAAPVPGPGPRSPQREPORVS 300  
QY 301 HEOFRALQLVVDGPGPRSYLDFIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQRR 360  
DB 301 HEOFRALQLVVDGPGPRSYLDFIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQRR 360

QY 361 ELLFNEVIMRDYQHENVEMVNSYLVGDELWVMEFLEGALTDIVTHRNMEQIAAV 420  
DB 361 ELLFNEVIMRDYQHENVEMVNSYLVGDELWVMEFLEGALTDIVTHRNMEQIAAV 420  
QY 421 CLAVALSVLAQVYIHRDIDKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKSLVGTPT 480  
DB 421 CLAVALSVLAQVYIHRDIDKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKSLVGTPT 480  
QY 481 WMAPELISRLPYGPEVDIWSLIGIMVEMVDGEPYPFNEPPLKAMKIRIIDLPPRLKNLHK 540  
DB 481 WMAPELISRLPYGPEVDIWSLIGIMVEMVDGEPYPFNEPPLKAMKIRIIDLPPRLKNLHK 540  
QY 541 VSPSLKGFIDRLVLRDPAQRATPAELIKHPFLAKAGPPASIVPLMRQNRTR 591  
DB 541 VSPSLKGFIDRLVLRDPAQRATPAELIKHPFLAKAGPPASIVPLMRQNRTR 591

## RESULT 5

US-10-893-025-5  
; Sequence 5, Application US/10893025  
; Publication No. US20050037965A1  
; GENERAL INFORMATION:  
; APPLICANT: Aventis Pharma Deutschland GmbH  
; APPLICANT: BARADEAU, Sebastian  
; APPLICANT: BARTNIK, Eckart  
; APPLICANT: CZECH, Joerg  
; APPLICANT: BLATT, Andreas  
; APPLICANT: LEBERER, Ekkehard  
; APPLICANT: LEBUW, Thomas  
; TITLE OF INVENTION: Use of a PAK Inhibitor for the Treatment of a Joint Disease  
; FILE REFERENCE: DEAY2003/0055 US NP  
; CURRENT APPLICATION NUMBER: US/10/893,025  
; CURRENT FILING DATE: 2004-07-16  
; PRIOR APPLICATION NUMBER: 60/527,819  
; PRIOR FILING DATE: 2003-12-08  
; PRIOR APPLICATION NUMBER: 03016306.4  
; PRIOR FILING DATE: 2004-07-18  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-893-025-5

Query Match 100.0%; Score 3090; DB 17; Length 591;  
Best Local Similarity 100.0%; Pred. No. 5.7e-161;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFGKRRKRVETISAPSNFHRVHTGPDQEQKFTGLPRQWQSLIEESARRPKPLVDPACIT 60  
DB 1 MFGKRRKRVETISAPSNFHRVHTGPDQEQKFTGLPRQWQSLIEESARRPKPLVDPACIT 60  
QY 61 STOPGAPKTIIVRSKAKGKAGLTLILDEFENMVSITNSLRDSDPPPPARAQENGMPEE 120  
DB 61 STOPGAPKTIIVRSKAKGKAGLTLILDEFENMVSITNSLRDSDPPPPARAQENGMPEE 120  
QY 121 PATTAGGPGKAGSRGRFAGHSEAGGSGDRRRAGPEKPKSRREGSGGPOESSRDKRPL 180  
DB 121 PATTAGGPGKAGSRGRFAGHSEAGGSGDRRRAGPEKPKSRREGSGGPOESSRDKRPL 180  
QY 181 SGPDVGTPOAGIAGAKLAAGRPFTTYPRADTDHPSRGAQGEPHDVAVNGPSAGGLAIP 240  
DB 181 SGPDVGTPOAGIAGAKLAAGRPFTTYPRADTDHPSRGAQGEPHDVAVNGPSAGGLAIP 240  
QY 241 QSSSSSSRPPTARAGAPSPGVLGPHASEPQLAPACTPAAPVPGPGPRSPQREPORVS 300  
DB 241 QSSSSSSRPPTARAGAPSPGVLGPHASEPQLAPACTPAAPVPGPGPRSPQREPORVS 300  
QY 301 HEOFRALQLVVDGPGPRSYLDFIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQRR 360  
DB 301 HEOFRALQLVVDGPGPRSYLDFIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQRR 360

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QY 361 ELLENVIMRDYQHENVVEMNSYLVGDELWVMEFLBEGALTDIVTHTRMNEBOIAAV 420
DB 361 ELLENVIMRDYQHENVVEMNSYLVGDELWVMEFLBEGALTDIVTHTRMNEBOIAAV 420
QY 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVYKSDPGFCQVSKVPRKRSIVGTPT 480
DB 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVYKSDPGFCQVSKVPRKRSIVGTPT 480
QY 481 WMABELISRLPYGPEVDIWSLGIWVIMVDEGPEPPYFNEPPLKAMKIRDNLPRLKNIHK 540
DB 481 WMABELISRLPYGPEVDIWSLGIWVIMVDEGPEPPYFNEPPLKAMKIRDNLPRLKNIHK 540
QY 541 VSPSLKGFIDRLIVRDPAPQATAAELKHPLAKGPPASIVPLMRONR 591
DB 541 VSPSLKGFIDRLIVRDPAPQATAAELKHPLAKGPPASIVPLMRONR 591

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## RESULT 6

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US-10-134-102-1
/ Sequence 1, Application US/10134102
/ Publication No. US20030186254A1
/ GENERAL INFORMATION:
/ APPLICANT: Melnick, Michael B.
/ APPLICANT: Moritz, Albrecht
/ APPLICANT: Comb, Michael J.
/ TITLE OF INVENTION: Regulation of HIV-Tat and Nef by the Pak4 kinase and its
/ FILE REFERENCE: CST-176 CIP
/ CURRENT APPLICATION NUMBER: US/10/134,102
/ PRIOR FILING DATE: 2002-04-29
/ PRIOR APPLICATION NUMBER: 09/750,457
/ PRIOR FILING DATE: 2000-12-28
/ PRIOR APPLICATION NUMBER: 60/173,939
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 588
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-134-102-1

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Query Match 99.5%; Score 3075; DB 14; Length 588;
Best Local Similarity 100.0%; Pred. No. 3,7e-160;
Matches 588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MFGKRRKRVISAPSNFHRVHTGPDQHQKFTGLPRWOSLIIESARPKPLVDPACT 60
DB 1 MFGKRRKRVISAPSNFHRVHTGPDQHQKFTGLPRWOSLIIESARPKPLVDPACT 60
QY 61 SIOPGAPKTIIVGSKAGKDGALTLLDEFENMSVTRNSLRDSDPPPARARQENGMDEE 120
DB 61 SIOPGAPKTIIVGSKAGKDGALTLLDEFENMSVTRNSLRDSDPPPARARQENGMDEE 120
QY 121 PATTAGGCGKAGSKRRFAGHSEAGGSGDRRRAPPEKRPKSSREGSGPQESSRDRPL 180
DB 121 PATTAGGCGKAGSKRRFAGHSEAGGSGDRRRAPPEKRPKSSREGSGPQESSRDRPL 180
QY 181 SGPDVGTQPPAGLAGAKLAAGRPFNTYPRADTHPSRGAQGEPHDVAEPNGPSAGLAI 240
DB 181 SGPDVGTQPPAGLAGAKLAAGRPFNTYPRADTHPSRGAQGEPHDVAEPNGPSAGLAI 240
QY 241 QSSSSSSRPPTARAGAPSPGVLPYHASEPOLAPACTPAAPAVGPPGPPSPQEPQV 300
DB 241 QSSSSSSRPPTARAGAPSPGVLPYHASEPOLAPACTPAAPAVGPPGPPSPQEPQV 300
QY 301 HEQFPAALQVLVDPDPSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQQR 360
DB 301 HEQFPAALQVLVDPDPSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQQR 360
QY 361 ELLENVIMRDYQHENVVEMNSYLVGDELWVMEFLBEGALTDIVTHTRMNEBOIAAV 420

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DB 361 ELLENVIMRDYQHENVVEMNSYLVGDELWVMEFLBEGALTDIVTHTRMNEBOIAAV 420
QY 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVYKSDPGFCQVSKVPRKRSIVGTPT 480
DB 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVYKSDPGFCQVSKVPRKRSIVGTPT 480
QY 481 WMABELISRLPYGPEVDIWSLGIWVIMVDEGPEPPYFNEPPLKAMKIRDNLPRLKNIHK 540
DB 481 WMABELISRLPYGPEVDIWSLGIWVIMVDEGPEPPYFNEPPLKAMKIRDNLPRLKNIHK 540
QY 541 VSPSLKGFIDRLIVRDPAPQATAAELKHPLAKGPPASIVPLMRON 588
DB 541 VSPSLKGFIDRLIVRDPAPQATAAELKHPLAKGPPASIVPLMRON 588

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## RESULT 7

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US-10-618-941-111
/ Sequence 111, Application US/10618941
/ Publication No. US2004019792A1
/ GENERAL INFORMATION:
/ APPLICANT: WHYTE, DAVID
/ APPLICANT: MANNING, GERARD
/ APPLICANT: CAENEPEEL, SEAN
/ TITLE OF INVENTION: NOVEL KINASES
/ FILE REFERENCE: 034536-0321
/ CURRENT APPLICATION NUMBER: US/10/618,941
/ PRIOR FILING DATE: 2003-07-15
/ PRIOR APPLICATION NUMBER: 60/395,632
/ NUMBER OF SEQ ID NOS: 143
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 111
/ LENGTH: 593
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-10-618-941-111

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```

Query Match 92.6%; Score 2860; DB 16; Length 593;
Best Local Similarity 92.6%; Pred. No. 2.1e-148;
Matches 550; Conservative 10; Mismatches 30; Indels 4; Gaps 2;

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QY 1 MFGKRRKRVISAPSNFHRVHTGPDQHQKFTGLPRWOSLIIESARPKPLVDPACT 60
DB 1 MFGKRRKRVISAPSNFHRVHTGPDQHQKFTGLPRWOSLIIESARPKPLVDPACT 60
QY 61 SIOPGAPKTIIVGSKAGKDGALTLLDEFENMSVTRNSLRDSDPPPARARQENGMDEE 120
DB 61 SIOPGAPKTIIVGSKAGKDGALTLLDEFENMSVTRNSLRDSDPPPARARQENGMDEE 120
QY 121 PATTAGGCGKAGSKRRFAGHSEAGGSGDRRRAPPEKRPKSSREGSGPQESSRDRPL 180
DB 121 PATTAGGCGKAGSKRRFAGHSEAGGSGDRRRAPPEKRPKSSREGSGPQESSRDRPL 180
QY 181 SGPDVGTQPPAGLAGAKLAAGRPFNTYPRADTHPSRGAQGEPHDVAEPNGPSAGLAI 240
DB 181 SGPDVGTQPPAGLAGAKLAAGRPFNTYPRADTHPSRGAQGEPHDVAEPNGPSAGLAI 240
QY 241 QSSSSSSRPPTARAGAPSPGVLPYHASEPOLAPACTPAAPAVGPPGPPSPQEPQV 300
DB 241 QSSSSSSRPPTARAGAPSPGVLPYHASEPOLAPACTPAAPAVGPPGPPSPQEPQV 300
QY 301 HEQFPAALQVLVDPDPSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQQR 360
DB 301 HEQFPAALQVLVDPDPSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQQR 360
QY 361 ELLENVIMRDYQHENVVEMNSYLVGDELWVMEFLBEGALTDIVTHTRMNEBOIAAV 420
DB 361 ELLENVIMRDYQHENVVEMNSYLVGDELWVMEFLBEGALTDIVTHTRMNEBOIAAV 420

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Qy	478	TPYMAPELISRLPYSPEDVISLGMVLEWDGSPFPENPEPLKAMQIIDLNPPLKN	537
Db	480	TPYMAPELISRLPYSPEDVISLGMVLEWDGSPFPENPEPLKAMQIIDLNPPLKN	539
Qy	538	LHKVSSGLKFLDRLLVRDPAQATAEALLKHPFLAKGPPASIVPLMKQRTR	591
Db	540	LHKVSSGLKFLDRLLVRDPAQATAEALLKHPFLTKGPPASIVPLMKQRTR	593

RESULT 8  
US-09-291-417-30

Query Match	67.1%	Score 2073	DB 10	Length 398	
Best Local Similarity	100.0%	Pred. No. 1.4e-105			
Matches 398	0	Mismatches 0	Indels 0	Gaps 0	

Qy	19	ASGAKLAAGP	FATTYRATLDHP	SRACQEPHDVA	PNGPSAGGLAI	POSSSSSSSR	PTPRA	253						
Db	1	ASGAKLAAGP	FATTYRATLDHP	SRACQEPHDVA	PNGPSAGGLAI	POSSSSSSSR	PTPRA	60						
Qy	254	RGAPSPGVLG	PHASEPOLA	PACTPAAPVP	PGPRSPOR	PCQVSHQ	RAALQ	113						
Db	61	RGAPSPGVLG	PHASEPOLA	PACTPAAPVP	PGPRSPOR	PCQVSHQ	RAALQ	120						
Qy	314	PGDPRSTL	DNFKITIGSG	TGIVCIATVR	SSGKLVAVK	KMDLRKQ	RELLFNE	VIIMRDY	373					
Db	121	PGDPRSTL	DNFKITIGSG	TGIVCIATVR	SSGKLVAVK	KMDLRKQ	RELLFNE	VIIMRDY	180					
Qy	374	QHENVVMN	NSYLVG	BELWVME	FLGGLAT	YIYHTH	TMNEBQ	LAACVLA	LOALSVLHA	433				
Db	181	QHENVVMN	NSYLVG	BELWVME	FLGGLAT	YIYHTH	TMNEBQ	LAACVLA	LOALSVLHA	240				
Qy	434	QGVYHRD	IKSDSIL	LTHDR	VKLSDP	GFAQVS	KEVPR	KSLVGT	PYMADEL	ISRLPYG	493			
Db	241	QGVYHRD	IKSDSIL	LTHDR	VKLSDP	GFAQVS	KEVPR	KSLVGT	PYMADEL	ISRLPYG	300			
Qy	494	PEVDIWS	LGI	MIEMV	DG	BPYP	FNEBP	LKAM	KMIR	DNTPRL	KLHKVSP	SLKGF	DLRL	553
Db	301	PEVDIWS	LGI	MIEMV	DG	BPYP	FNEBP	LKAM	KMIR	DNTPRL	KLHKVSP	SLKGF	DLRL	360
Qy	554	VRDPAQ	RAAT	AAELLK	HP	FLAKA	GP	PAIS	YPL	RQR	NR	591		
Db	361	VRDPAQ	RAAT	AAELLK	HP	FLAKA	GP	PAIS	YPL	RQR	NR	398		

RESULT 9  
US-10-331-095-2  
; Sequence 2, Application US/10331095  
; Publication No. US20030124107A1  
; GENERAL INFORMATION:  
; APPLICANT: Columbia University  
; APPLICANT: Minden, Audrey  
; TITLE OF INVENTION: PAKS-Related Compositions and Methods  
; FILE REFERENCE: 0575/6/4083-A

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1  CURRENT APPLICATION NUMBER: US/10/331,095-2
2  CURRENT FILING DATE: 2002-12-27
3  PRIOR APPLICATION NUMBER: 60/343,972
4  PRIOR FILING DATE: 2001-12-28
5  NUMBER OF SEQ ID NOS: 6
6  SOFTWARE: PatentIn version 3.1
7  SEQ ID NO: 2
8  LENGTH: 719
9  TYPE: PRT
10 ORGANISM: mouse
11 FEATURE:
12 NAME/KEY: MISC_FEATURE
13 OTHER INFORMATION: mouse PAKS
14 US-10-331-095-2

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Query Match	56.68	Score 1748	DB 14	Length 719
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Best Local Similarity 52.9%; Pred. NO. 1.4e-8//  
Matches 385; Conservative 65; Mismatches 128; Indels 150; Gaps 16;

QY	1	MEFKRKRRVET	SAPNSFEHRVHTGDDQHEOKFTGLPRWOSLIESASRRPEPLVDPACIT	60
Db	1	MEFKKKKKKEI	ESGPSNFEHRVHTGDFDPEOKFTGLPQOMHSLADLTANRPKPMWDPSGIT	60
QY	61	STOPGAPKTI	VGSKGAKODGALTLLDEFENNSVTRSNLSRDSPPPP--ARAR-----	112
Db	61	PIQAPMKTI	IVGNKSKCKETSINGLLEDFDNI SVTRSNLSRKESPPPPDDGAASRLIOGHS	120
QY	113	QENGM-----	PEEPATTAGRGPGAGSRGNFA-----GH-----	141
Db	121	EENGFITFSQ	YSSESPTTADYTTEKRYRDSLYGDDLDLYKSHAAKONGHAMKMKHGA	180
QY	142	-----	SEAGGSGGDRRA-----	154
Db	181	YFEMKSLKTD	LAFGVYHTHLDLRKSSSEYGLDRMDYQASSSSPUDYSFOLTTPERTA	240
QY	155	-----	GP-----EKRPKSSREGSGGQFQESSRDKRPLSGEVDGTP--QPA	190
Db	241	GTSGCSKES	LAYSESDWPGLDDYDRPKSGLHQTSPQAMR--QKSKSGGLQEPMPMF	239
QY	192	GLASGAKLA	GRPFNTY-----PRADTDH-----PSRQAGEPHDVAANGP	232
Db	300	GAGAFPTHQ	GHSYNSVTYPLRSEPTMCI PKVDYDRAQWVSPPLSGS-----DTYPRGP	354
QY	233	SAGGLAIPOS	-----SSSSSRPPRARGA-----PSGVLGPHASEPOLAPRACTAPAR	281
Db	355	T-----	KLPOSQAKAGYSSGSHQYEGCHKASLYHHPSLQTSOYITRASYL--SEL5ISS	409
QY	282	AVPGPGRPS	PQREPORVSHQFRAALQLVDPGDPGRSYLDMFKIEGSGTGIYCIATVR	341
Db	410	TYPRPBGSS	SQOQRPVRSHQFRAALQLVSPGDPGRYLDNFKIEGSGTGIYCIATEK	459
QY	342	SSGKLVAVK	KMDLRKQORRELLFNEVIMRDYQHENVEMTNSYLVGDDELAVMEPLEGG	401
Db	470	HTGQVAVK	KMDLRKQORRELLFNEVIMRDYHDNDVDMTNSYLVGDDELAVMEPLEGG	529
QY	402	ALTDIYTHR	NMEQJLAACLAIVQALSVLAQCIYHDIKDSILLTHGRRVYLSDPGF	461
Db	530	ALTDIYTHR	NMEQJLAATCLSVLAALSYLHNQCIYHDIKDSILLTHSDRIKLSDFGF	569
QY	462	CAQVSKEVP	RKSLVGTPYMAPELISRLPGYEPVDIMSLGIWYIEMWDGSPYFNEPPL	521
Db	590	CAQVSKEVP	RKSLVGTPTMAPEVYISLPLGTETVDIMSLGIWYIEMWDGSPYFNEPPL	649
QY	522	KAMKMI	RDNLPRPLKNLKHVSPSLKGLIDRLLVDPDQATRAELKHPLAKGAPPAST	561
Db	650	QAMRRIRDS	LPRVXOLHKVSSMLGFLDMLVPEPSQATRAOBLGHPLKLAGPSPCI	709
QY	582	VPLMRQNR	589	
Db	710	VPLMRQYR	717	

## RESULT 10

US-10-331-095-4  
; Sequence 4, Application US/10331095  
; Publication No. US20030124107A1  
; GENERAL INFORMATION:  
; APPLICANT: Columbia University  
; APPLICANT: Manden, Audrey  
; TITLE OF INVENTION: PAKS-Related Compositions and Methods  
; FILE REFERENCE: 0575/64083-A  
; CURRENT APPLICATION NUMBER: US/10/331,095  
; PRIOR FILING DATE: 2002-12-27  
; PRIOR APPLICATION NUMBER: 60/343,972  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: human  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; OTHER INFORMATION: Human PAKS  
US-10-331-095-4

Query Match 56.0%; Score 1731; DB 14; Length 719;  
Best Local Similarity 52.4%; Pred. No. 1.2e-86;  
Matches 383; Conservative 66; Mismatches 126; Indels 156; Gaps 17;

QY 1 MFGKKRKRVEISAPSNFHRVHTGPDQHEQKFTGLPRQWOSLIESARPKPLVDPACT 60  
DB 1 MFGKKKKKRIEISGNSFHRVHTGPDQHEQKFTGLPRQWOSLIESARPKPLVDPACT 60  
QY 61 SIQGAPKTIYRSGKAKDGLTLTLLDEFENMSTYNSLRDSEPPPARA-----R 112  
DB 61 PIQAPKTIYRSGKAKDGLTLTLLDEFENMSTYNSLRDSEPPPARA-----R 112  
QY 113 QENGM-----PEEPATTA-----RGG-----PGKA 132  
DB 121 EENGFITFSQYSSESDTTADYTTEKYREKSLYGDLDLPYRKSHAKONGHVMKMGHEA 180  
QY 133 -----GSRGPFAGH-----SEAG 145  
DB 181 YSEVYPLKSDPAFADYHSHLDSLSPSEYSDLMKEYORASSSPLDYSGFTPSRTA 240  
QY 146 GSGGDRRA-----GP-----EKRPKSRSGSGPOESSRDKRPLSGPDVGT-OPA 191  
DB 241 GTSGCSKESLAVSEBWPGLDDYDRPKSYLANTSTPQTR-QRSRSGSLQEPMPMF 299  
QY 192 GLASGAKLAAGRPNTY-----PRADTDH-----PSRGAQGEPHDVAENGP 232  
DB 300 GASAFTHPQGHSTYNSYTYPRLSEPTMCI PKVDYDRAQWVLSPLSGS-----DTYRGP 354  
QY 233 SAGGLAIPOS-----SSSSSRPPTRAGAPSPVGLGPHASEPOLAPACTP----- 278  
DB 355 A-----KLPOSQSKSGYSSSSHQYPSGYNKA-----TLYHHPQLQSSSQYISTASYLSLSL 406  
QY 279 AAPAVGPPGPRSPQREPORVSHQFRAALQLVDPDPRSYLDNFIKIGESTGIYCIA 338  
DB 407 SSSYTPPSPWSSSDQPSRVSHQFRAALQLVSPDPREYLANFIKIGESTGIYCIA 466  
QY 339 TVRSSGKLVAVKMDLKRQORRELLFNEVIMTDYGHENYEMNSTYLVDGLVVMVEFL 398  
DB 467 TEKHTGKQVAVKMDLKRQORRELLFNEVIMTDYGHENYEMNSTYLVDGLVVMVEFL 526  
QY 399 EGGLALTDIVTTRNNEQIAVCLAVLQALSVLAQGVIRHDIKSDSILLTHDGRVYKLS 458  
DB 527 EGGLALTDIVTTRNNEQIAVCLAVLQALSVLAQGVIRHDIKSDSILLTHDGRVYKLS 586  
QY 459 FGFCAGVSKVPRKSLVGTIPYMAPELISRLPYGPEVDIWSLGIWIEVDGEPPYFNE 518  
DB 587 FGFCAGVSKVPRKSLVGTIPYMAPELISRLPYGPEVDIWSLGIWIEVDGEPPYFNE 646  
QY 519 PPLQAMKRIKIDSLPRVKDLHKVSVLRGFLDMLVREPSORATAQELLGHPFLKLAGPP 578

DB 647 PPLQAMKRIKIDSLPRVKDLHKVSVLRGFLDMLVREPSORATAQELLGHPFLKLAGPP 706  
QY 579 ASIYPLMRQNR 589  
DB 707 SCIVPLMRQYR 717  
RESULT 11  
US-10-394-322A-49  
; Sequence 49, Application US/10394322A  
; Publication No. US20030232391A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNEIS PHARMACEUTICALS, INC.  
; APPLICANT: Prescott, John C.  
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS  
; FILE REFERENCE: 39750-0006 US  
; CURRENT APPLICATION NUMBER: US/10/394,322A  
; PRIOR FILING DATE: 2003-03-20  
; PRIOR APPLICATION NUMBER: US 60/366,892  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 49  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-394-322A-49

Query Match 56.0%; Score 1731; DB 15; Length 719;  
Best Local Similarity 52.4%; Pred. No. 1.2e-86;  
Matches 383; Conservative 66; Mismatches 126; Indels 156; Gaps 17;

QY 1 MFGKKRKRVEISAPSNFHRVHTGPDQHEQKFTGLPRQWOSLIESARPKPLVDPACT 60  
DB 1 MFGKKKKKRIEISGNSFHRVHTGPDQHEQKFTGLPRQWOSLIESARPKPLVDPACT 60  
QY 61 SIQGAPKTIYRSGKAKDGLTLTLLDEFENMSTYNSLRDSEPPPARA-----R 112  
DB 61 PIQAPKTIYRSGKAKDGLTLTLLDEFENMSTYNSLRDSEPPPARA-----R 112  
QY 113 QENGM-----PEEPATTA-----RGG-----PGKA 132  
DB 121 EENGFITFSQYSSESDTTADYTTEKYREKSLYGDLDLPYRKSHAKONGHVMKMGHEA 180  
QY 133 -----GSRGPFAGH-----SEAG 145  
DB 181 YSEVYPLKSDPAFADYHSHLDSLSPSEYSDLMKEYORASSSPLDYSGFTPSRTA 240  
QY 146 GSGGDRRA-----GP-----EKRPKSRSGSGPOESSRDKRPLSGPDVGT-OPA 191  
DB 241 GTSGCSKESLAVSEBWPGLDDYDRPKSYLANTSTPQTR-QRSRSGSLQEPMPMF 299  
QY 192 GLASGAKLAAGRPNTY-----PRADTDH-----PSRGAQGEPHDVAENGP 232  
DB 300 GASAFTHPQGHSTYNSYTYPRLSEPTMCI PKVDYDRAQWVLSPLSGS-----DTYRGP 354  
QY 233 SAGGLAIPOS-----SSSSSRPPTRAGAPSPVGLGPHASEPOLAPACTP----- 278  
DB 355 A-----KLPOSQSKSGYSSSSHQYPSGYNKA-----TLYHHPQLQSSSQYISTASYLSLSL 406  
QY 279 AAPAVGPPGPRSPQREPORVSHQFRAALQLVDPDPRSYLDNFIKIGESTGIYCIA 338  
DB 407 SSSYTPPSPWSSSDQPSRVSHQFRAALQLVSPDPREYLANFIKIGESTGIYCIA 466  
QY 339 TVRSSGKLVAVKMDLKRQORRELLFNEVIMTDYGHENYEMNSTYLVDGLVVMVEFL 398  
DB 467 TEKHTGKQVAVKMDLKRQORRELLFNEVIMTDYGHENYEMNSTYLVDGLVVMVEFL 526  
QY 399 EGGLALTDIVTTRNNEQIAVCLAVLQALSVLAQGVIRHDIKSDSILLTHDGRVYKLS 458  
DB 527 EGGLALTDIVTTRNNEQIAVCLAVLQALSVLAQGVIRHDIKSDSILLTHDGRVYKLS 586  
QY 459 FGFCAGVSKVPRKSLVGTIPYMAPELISRLPYGPEVDIWSLGIWIEVDGEPPYFNE 518

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Db      587  FEGCAVSKVEPRKSLVGPYMADEVSRLLPYGTEVDIMSLGIVIMIDSEPPYFHE 646
        519  PPLKAMKMTIDNLPPLKMLHKVSPSLKGFLLDRLVDPAPQATYAAELLKHPFLAVAGPP 578
        647  PPLQAMRRIRDSLPPIVKDLHKVSVLRGFLDMLVREPSQATQELLGHPFLKLAGPP 706
Qy      579  ASIVPLMRQNR 589
        707  SCTIVPLMRQYR 717

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## RESULT 12

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US-10-406-676-5
; Sequence 5, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Anthonyamy, Stephen
; APPLICANT: Fell, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-676-5

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Query Match      48.6%; Score 1502; DB 15; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.5e-74;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      300  SHEQFPAALQLVYDPPGDSYLDNFKIGEGSTGIVCIATVRSNGKLVAVKMDLRKQOR 359
        1  SHEQFPAALQLVYDPPGDSYLDNFKIGEGSTGIVCIATVRSNGKLVAVKMDLRKQOR 60
Db      360  RELLFNEVYIMRDYQHENYVENYNSYLVDDELVMVMEFEGGALTDIIVHTTRMNEQIAA 419
        61  RELLFNEVYIMRDYQHENYVENYNSYLVDDELVMVMEFEGGALTDIIVHTTRMNEQIAA 120
Qy      420  VCLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVYLSDFGCAQVSKVEPRKSLVGT 479
        121  VCLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVYLSDFGCAQVSKVEPRKSLVGT 180
Db      480  YMAPELISRLPYGPEVDIWSLGINVYIEMVDGEPFYFNEBPPLKAMKMTIDNLPPLKNTL 539
        181  YMAPELISRLPYGPEVDIWSLGINVYIEMVDGEPFYFNEBPPLKAMKMTIDNLPPLKNTL 240
Qy      540  KVSPLSKGFLDRLVDPAPQATYAAELLKHPFLAKGPPASIVPLMRQNR 591
        241  KVSPLSKGFLDRLVDPAPQATYAAELLKHPFLAKGPPASIVPLMRQNR 292
Db

```

## RESULT 13

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US-10-406-676-6
; Sequence 6, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Anthonyamy, Stephen

```

```

; APPLICANT: Fell, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-676-6

```

```

Query Match      48.6%; Score 1502; DB 15; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.5e-74;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      300  SHEQFPAALQLVYDPPGDSYLDNFKIGEGSTGIVCIATVRSNGKLVAVKMDLRKQOR 359
        1  SHEQFPAALQLVYDPPGDSYLDNFKIGEGSTGIVCIATVRSNGKLVAVKMDLRKQOR 60
Db      360  RELLFNEVYIMRDYQHENYVENYNSYLVDDELVMVMEFEGGALTDIIVHTTRMNEQIAA 419
        61  RELLFNEVYIMRDYQHENYVENYNSYLVDDELVMVMEFEGGALTDIIVHTTRMNEQIAA 120
Qy      420  VCLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVYLSDFGCAQVSKVEPRKSLVGT 479
        121  VCLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVYLSDFGCAQVSKVEPRKSLVGT 180
Db      480  YMAPELISRLPYGPEVDIWSLGINVYIEMVDGEPFYFNEBPPLKAMKMTIDNLPPLKNTL 539
        181  YMAPELISRLPYGPEVDIWSLGINVYIEMVDGEPFYFNEBPPLKAMKMTIDNLPPLKNTL 240
Qy      540  KVSPLSKGFLDRLVDPAPQATYAAELLKHPFLAKGPPASIVPLMRQNR 591
        241  KVSPLSKGFLDRLVDPAPQATYAAELLKHPFLAKGPPASIVPLMRQNR 292
Db

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## RESULT 14

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US-10-406-676-8
; Sequence 8, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Anthonyamy, Stephen
; APPLICANT: Fell, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 292
; TYPE: PRT

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ORGANISM: H.sapiens  
US-10-406-676-8

Query Match 48.6%; Score 1502; DB 15; Length 292;  
Best Local Similarity 100.0%; Pred. No. 1.5e-74;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 SHEQFRALQLVDPGPRSYLDFIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQOR 359  
DB 1 SHEQFRALQLVDPGPRSYLDFIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQOR 60  
QY 360 RELLFNEVIMRDYQHENVVEMVNSYLVDGLWVMEFLGALTDIVTHTRMNEEQIAA 419  
DB 61 RELLFNEVIMRDYQHENVVEMVNSYLVDGLWVMEFLGALTDIVTHTRMNEEQIAA 120  
QY 420 VCLAVLQALSVLHAGVYIHRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSIVGTP 479  
DB 121 VCLAVLQALSVLHAGVYIHRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSIVGTP 180  
QY 480 YMAAPELISRLPYGPEVDIWSLGIWVIEWVDGEPYFNEPPLKAMKMIKRDNLPRRLKNLH 539  
DB 181 YMAAPELISRLPYGPEVDIWSLGIWVIEWVDGEPYFNEPPLKAMKMIKRDNLPRRLKNLH 240  
QY 540 KVSPSLKGFLDRLVDPDPAQRATAELKHPFLAKAGPPASIVPLMRQNRTR 591  
DB 241 KVSPSLKGFLDRLVDPDPAQRATAELKHPFLAKAGPPASIVPLMRQNRTR 292

## RESULT 15

US-10-406-676-9  
Sequence 9, Application US/10406676  
Publication No. US20030229453A1  
GENERAL INFORMATION:  
APPLICANT: Structural Genomix, Inc.  
APPLICANT: Antonyamy, Stephen  
APPLICANT: Feil, Ingeborg  
APPLICANT: Buchanan, Sean  
APPLICANT: Post, Kai W.  
APPLICANT: Liu, Yi  
APPLICANT: Lorber, David  
TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4D KINASE  
FILE REFERENCE: 524982002300  
CURRENT APPLICATION NUMBER: US/10/406,676  
PRIOR FILING DATE: 2003-04-02  
PRIOR APPLICATION NUMBER: 60/371,018  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/430,567  
PRIOR FILING DATE: 2002-12-02  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FaastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 292  
TYPE: PRT  
ORGANISM: H.sapiens  
US-10-406-676-9

Query Match 48.6%; Score 1502; DB 15; Length 292;  
Best Local Similarity 100.0%; Pred. No. 1.5e-74;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 SHEQFRALQLVDPGPRSYLDFIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQOR 359  
DB 1 SHEQFRALQLVDPGPRSYLDFIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQOR 60  
QY 360 RELLFNEVIMRDYQHENVVEMVNSYLVDGLWVMEFLGALTDIVTHTRMNEEQIAA 419  
DB 61 RELLFNEVIMRDYQHENVVEMVNSYLVDGLWVMEFLGALTDIVTHTRMNEEQIAA 120  
QY 420 VCLAVLQALSVLHAGVYIHRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSIVGTP 479  
DB 121 VCLAVLQALSVLHAGVYIHRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSIVGTP 180

QY 480 YMAAPELISRLPYGPEVDIWSLGIWVIEWVDGEPYFNEPPLKAMKMIKRDNLPRRLKNLH 539  
DB 181 YMAAPELISRLPYGPEVDIWSLGIWVIEWVDGEPYFNEPPLKAMKMIKRDNLPRRLKNLH 240  
QY 540 KVSPSLKGFLDRLVDPDPAQRATAELKHPFLAKAGPPASIVPLMRQNRTR 591  
DB 241 KVSPSLKGFLDRLVDPDPAQRATAELKHPFLAKAGPPASIVPLMRQNRTR 292

Search completed: March 15, 2005, 11:47:58  
Job time : 162.787 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: March 15, 2005, 11:18:02 ; Search time 52.1471 Seconds

(without alignments)  
846.023 Million cell updates/sec

Title: US-10-693-367-2

Perfect score: 3090

Sequence: 1 MGRKKRKRVEISAPSNFEHR.....LAKAGPAPSIPLMQRNR 591

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/prodata/1/1aa/6CTUS\_COMB.pep:\*
- 6: /cgn2\_6/prodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3090	100.0	591	3	US-09-082-737-2
2	3090	100.0	591	4	US-09-688-188B-103
3	3090	100.0	591	4	US-09-718-032-2
4	3090	100.0	591	4	US-09-291-417D-103
5	3090	100.0	591	4	US-09-949-016-6665
6	3090	100.0	620	4	US-09-949-016-7206
7	2073	67.1	398	4	US-09-688-188B-30
8	2073	67.1	398	4	US-09-291-417D-30
9	1473.5	47.7	681	4	US-09-688-188B-29
10	1473.5	47.7	681	4	US-09-291-417D-29
11	1473.5	47.7	694	4	US-09-949-016-10445
12	1470.5	47.6	681	4	US-09-765-815-2
13	1277	41.3	250	3	US-09-082-737-3
14	1277	41.3	250	4	US-09-718-032-3
15	912	29.5	544	2	US-08-935-760-2
16	909	29.4	544	4	US-09-949-016-11562
17	907	29.4	544	4	US-09-688-188B-95
18	904	29.3	544	4	US-09-291-417D-95
19	904	29.3	524	4	US-09-538-092-1301
20	900	29.1	524	2	US-08-615-942A-2
21	900	29.1	524	4	US-09-237-325-2
22	899	29.1	544	3	US-08-559-397A-19
23	894	28.9	506	1	US-08-369-780-2
24	894	28.9	506	1	US-08-475-682-2
25	894	28.9	506	1	US-08-780-833-2
26	894	28.9	506	1	US-08-636-036-2
27	894	28.9	506	3	US-08-918-509-2

28	894	28.9	506	3	US-09-108-262-2	Sequence 2, App1
29	894	28.9	506	4	US-09-688-188B-94	Sequence 94, App1
30	894	28.9	506	4	US-09-291-417D-94	Sequence 94, App1
31	893.5	28.9	551	4	US-09-949-016-10951	Sequence 10951, A
32	892.5	28.9	545	4	US-09-538-092-1297	Sequence 1297, Ap
33	891.5	28.9	545	2	US-08-935-760-4	Sequence 4, App1
34	891.5	28.9	545	4	US-09-688-188B-93	Sequence 93, App1
35	891.5	28.9	545	4	US-09-291-417D-93	Sequence 93, App1
36	867	28.1	544	3	US-08-559-397A-29	Sequence 29, App1
37	849	27.5	544	3	US-08-559-397A-30	Sequence 30, App1
38	833.5	27.0	465	2	US-08-114-555A-2	Sequence 2, App1
39	821	26.6	694	3	US-08-559-397A-31	Sequence 31, App1
40	814.5	26.4	465	3	US-08-559-397A-2	Sequence 2, App1
41	804	26.0	305	4	US-09-765-815-10	Sequence 10, App1
42	782	25.3	793	3	US-09-588-256-10	Sequence 10, App1
43	769	24.9	268	2	US-08-852-743-3	Sequence 3, App1
44	769	24.9	268	3	US-09-185-370-3	Sequence 3, App1
45	755	24.4	410	4	US-09-248-796A-18461	Sequence 18461, A

## ALIGNMENTS

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RESULT 1
US-09-082-737-2
; Sequence 2, Application US/09082737
; Patent No. 6013500
; GENERAL INFORMATION:
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK; A No. 6013500el Gene Encoding A Serine/
; NUMBER OF INVENTION: Threonine Kinase
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11230
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,737
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/55311
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ. ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-082-737-2
Query Match 100.0%; Score 3090; DB 3; Length 591;
Best local Similarity 100.0%; Pred. No. 3e-191;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGRKKRKRVEISAPSNFEHRVHTGPDHOKXTGLPRQWOSLIESARPKPLVDPACTT 60
DB 1 MGRKKRKRVEISAPSNFEHRVHTGPDHOKXTGLPRQWOSLIESARPKPLVDPACTT 60
QY 61 STPGAPKTIIVGSKAKGALTLLDDEFENNSVTSNLSLRDSDPPPARAQENGMPEE 120
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Db 61 SIOPGAPKTIYVSGKAGDGLTLLDDEFENMSVTRNSLRDSEPPPARAQENGME 120  
QY 121 PATTARGGPGKAGSGRPAHSEAGGSGDRRRAGPEKRPKSREGSGGPOESSRDKRL 180  
Db 121 PATTARGGPGKAGSGRPAHSEAGGSGDRRRAGPEKRPKSREGSGGPOESSRDKRL 180  
QY 181 SGPVGTGPAGIAGSAGAKIAGRPNTYPRADTHPSRGAQGEHPDVA PNGPSAGLAIP 240  
Db 181 SGPVGTGPAGIAGSAGAKIAGRPNTYPRADTHPSRGAQGEHPDVA PNGPSAGLAIP 240  
QY 241 QSSSSSRPPTARAGAPSPGVLAGPHASEPOLAPACTPAAPAVPPEPPRSPQREPORVS 300  
Db 241 QSSSSSRPPTARAGAPSPGVLAGPHASEPOLAPACTPAAPAVPPEPPRSPQREPORVS 300  
QY 301 HEQFRALQIYVDPGDPSPSYLDFNFIKIGSGTGIVCIATVRSSEGLVAVKMDLRKQOR 360  
Db 301 HEQFRALQIYVDPGDPSPSYLDFNFIKIGSGTGIVCIATVRSSEGLVAVKMDLRKQOR 360  
QY 361 ELLENVYIMRDYQHENNVEMVNSYLVGDELMVMEFLGEGALTDIVTHTRMNEBOIAV 420  
Db 361 ELLENVYIMRDYQHENNVEMVNSYLVGDELMVMEFLGEGALTDIVTHTRMNEBOIAV 420  
QY 421 CLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVYKLSDFGCAQVSKVPRKSLVGTPI 480  
Db 421 CLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVYKLSDFGCAQVSKVPRKSLVGTPI 480  
QY 481 WMAPELISRLPYGPEVDIWSLGIMVIEVNDGEPPEYFNEPPLKAMKMTI RDLNLPRLKNLHK 540  
Db 481 WMAPELISRLPYGPEVDIWSLGIMVIEVNDGEPPEYFNEPPLKAMKMTI RDLNLPRLKNLHK 540  
QY 541 VSPSLKGFIDRLILVRDPAQRATAELKHPFLAKAGPASIYVLMKRONRTR 591  
Db 541 VSPSLKGFIDRLILVRDPAQRATAELKHPFLAKAGPASIYVLMKRONRTR 591

RESULT 2  
US-09-688-188B-103  
/ Sequence 103, Application US/09688188B  
/ Patent No. 6656716  
/ GENERAL INFORMATION:  
/ APPLICANT: PLOOMMAN, GREGORY  
/ APPLICANT: MARTINEZ, RICARDO  
/ APPLICANT: WHYTE, DAVID  
/ TITLE OF INVENTION: STEZO-RELATED PROTEIN KINASES  
/ FILE REFERENCE: 038602/0328  
/ CURRENT APPLICATION NUMBER: US/09/688,188B  
/ PRIOR FILING DATE: 2000-10-16  
/ PRIOR APPLICATION NUMBER: 09/291,417  
/ PRIOR FILING DATE: 1999-04-14  
/ PRIOR APPLICATION NUMBER: 60/081,784  
/ NUMBER OF SEQ ID NOS: 155  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO: 103  
/ LENGTH: 591  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-09-688-188B-103

Query Match 100.0%; Score 3090; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 3e-191;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFGKRRKVEISAPSNFEHRVHTGFDHOKFTGLPRQMSLIIESARRKPLVDPACT 60  
Db 1 MFGKRRKVEISAPSNFEHRVHTGFDHOKFTGLPRQMSLIIESARRKPLVDPACT 60  
QY 61 SIOPGAPKTIYVSGKAGDGLTLLDDEFENMSVTRNSLRDSEPPPARAQENGME 120  
Db 61 SIOPGAPKTIYVSGKAGDGLTLLDDEFENMSVTRNSLRDSEPPPARAQENGME 120  
QY 121 PATTARGGPGKAGSGRPAHSEAGGSGDRRRAGPEKRPKSREGSGGPOESSRDKRL 180  
Db 121 PATTARGGPGKAGSGRPAHSEAGGSGDRRRAGPEKRPKSREGSGGPOESSRDKRL 180

Db 121 PATTARGGPGKAGSGRPAHSEAGGSGDRRRAGPEKRPKSREGSGGPOESSRDKRL 180  
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Db 181 SGPVGTGPAGIAGSAGAKIAGRPNTYPRADTHPSRGAQGEHPDVA PNGPSAGLAIP 240  
QY 241 QSSSSSRPPTARAGAPSPGVLAGPHASEPOLAPACTPAAPAVPPEPPRSPQREPORVS 300  
Db 241 QSSSSSRPPTARAGAPSPGVLAGPHASEPOLAPACTPAAPAVPPEPPRSPQREPORVS 300  
QY 301 HEQFRALQIYVDPGDPSPSYLDFNFIKIGSGTGIVCIATVRSSEGLVAVKMDLRKQOR 360  
Db 301 HEQFRALQIYVDPGDPSPSYLDFNFIKIGSGTGIVCIATVRSSEGLVAVKMDLRKQOR 360  
QY 361 ELLENVYIMRDYQHENNVEMVNSYLVGDELMVMEFLGEGALTDIVTHTRMNEBOIAV 420  
Db 361 ELLENVYIMRDYQHENNVEMVNSYLVGDELMVMEFLGEGALTDIVTHTRMNEBOIAV 420  
QY 421 CLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVYKLSDFGCAQVSKVPRKSLVGTPI 480  
Db 421 CLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVYKLSDFGCAQVSKVPRKSLVGTPI 480  
QY 481 WMAPELISRLPYGPEVDIWSLGIMVIEVNDGEPPEYFNEPPLKAMKMTI RDLNLPRLKNLHK 540  
Db 481 WMAPELISRLPYGPEVDIWSLGIMVIEVNDGEPPEYFNEPPLKAMKMTI RDLNLPRLKNLHK 540  
QY 541 VSPSLKGFIDRLILVRDPAQRATAELKHPFLAKAGPASIYVLMKRONRTR 591  
Db 541 VSPSLKGFIDRLILVRDPAQRATAELKHPFLAKAGPASIYVLMKRONRTR 591

RESULT 3  
US-09-718-032-2  
/ Sequence 2, Application US/09718032  
/ Patent No. 6667168  
/ GENERAL INFORMATION:  
/ APPLICANT: The Trustees of Columbia University  
/ APPLICANT: Minden, Audrey  
/ TITLE OF INVENTION: PAK4, A NOVEL GENE ENDODING A SERINE/THREONINE KINASE  
/ FILE REFERENCE: 575/55311-A-PCT-US  
/ CURRENT APPLICATION NUMBER: US/09/718,032  
/ PRIOR FILING DATE: 2000-11-21  
/ PRIOR APPLICATION NUMBER: PCT/US99/11341  
/ PRIOR FILING DATE: 1999-05-21  
/ PRIOR APPLICATION NUMBER: 09/082,737  
/ NUMBER OF SEQ ID NOS: 17  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO: 2  
/ LENGTH: 591  
/ TYPE: PRT  
/ ORGANISM: human  
US-09-718-032-2

Query Match 100.0%; Score 3090; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 3e-191;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFGKRRKVEISAPSNFEHRVHTGFDHOKFTGLPRQMSLIIESARRKPLVDPACT 60  
Db 1 MFGKRRKVEISAPSNFEHRVHTGFDHOKFTGLPRQMSLIIESARRKPLVDPACT 60  
QY 61 SIOPGAPKTIYVSGKAGDGLTLLDDEFENMSVTRNSLRDSEPPPARAQENGME 120  
Db 61 SIOPGAPKTIYVSGKAGDGLTLLDDEFENMSVTRNSLRDSEPPPARAQENGME 120  
QY 121 PATTARGGPGKAGSGRPAHSEAGGSGDRRRAGPEKRPKSREGSGGPOESSRDKRL 180  
Db 121 PATTARGGPGKAGSGRPAHSEAGGSGDRRRAGPEKRPKSREGSGGPOESSRDKRL 180  
QY 181 SGPVGTGPAGIAGSAGAKIAGRPNTYPRADTHPSRGAQGEHPDVA PNGPSAGLAIP 240  
Db 181 SGPVGTGPAGIAGSAGAKIAGRPNTYPRADTHPSRGAQGEHPDVA PNGPSAGLAIP 240

QY 241 QSSSSSRPTTRAGAPSPGVLGPHASEPOLAPACTPAAPVGPGRPSRORFORVS 300  
DB 241 QSSSSSRPTTRAGAPSPGVLGPHASEPOLAPACTPAAPVGPGRPSRORFORVS 300  
QY 301 HEQFRAALQLVDPGPRSYLNDNFIKIGSGTGVCIATVRSRSGKLVAVKMDLRKQRR 360  
DB 301 HEQFRAALQLVDPGPRSYLNDNFIKIGSGTGVCIATVRSRSGKLVAVKMDLRKQRR 360  
QY 361 ELLFNEVIMRDYOHENNVEMNSYLVDGLVWMEFLLEGALTDIVTTRNMEQIAAV 420  
DB 361 ELLFNEVIMRDYOHENNVEMNSYLVDGLVWMEFLLEGALTDIVTTRNMEQIAAV 420  
QY 421 CLAVALQALSVLAQGVYIHRDIKSDSILLTHDGRVYKLSDFGCAQVSKVPRKSLVGTPT 480  
DB 421 CLAVALQALSVLAQGVYIHRDIKSDSILLTHDGRVYKLSDFGCAQVSKVPRKSLVGTPT 480  
QY 481 WMAPELISRLPYGPEVDIMSLGIMVLEWVDEPPYFNEPPLKAMKIRDLNLPRLKNLHK 540  
DB 481 WMAPELISRLPYGPEVDIMSLGIMVLEWVDEPPYFNEPPLKAMKIRDLNLPRLKNLHK 540  
QY 541 VSPSLKGFDRLLVRDPAQRATPAELIKHPFLAKAGPPASIVPLMRQNRTR 591  
DB 541 VSPSLKGFDRLLVRDPAQRATPAELIKHPFLAKAGPPASIVPLMRQNRTR 591  
RESULT 4  
US-09-291-417D-103  
; Sequence 103, Application US/09291417D  
; Patent No. 6680170  
; GENERAL INFORMATION:  
; APPLICANT: PIOMMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHITE, DAVID  
; TITLE OF INVENTION: STEZO-RELATED PROTEIN KINASES  
; FILE REFERENCE: 038602/0329  
; CURRENT APPLICATION NUMBER: US/09/291,417D  
; CURRENT FILING DATE: 1999-04-13  
; PRIOR APPLICATION NUMBER: 60/081,784  
; PRIOR FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 103  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-291-417D-103  
Query Match 100.0%; Score 3090; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 3e-191;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFGKRRKRVISAPSNFEHVRHTGPDHOKFTGLPRWOSLIIESARRPKPLVDPACTT 60  
DB 1 MFGKRRKRVISAPSNFEHVRHTGPDHOKFTGLPRWOSLIIESARRPKPLVDPACTT 60  
QY 61 SIOPGAPKTIIVGSKAKDGLTLLDDEFENMSVTRSNLSLRDSDPPPARAQENGMPEE 120  
DB 61 SIOPGAPKTIIVGSKAKDGLTLLDDEFENMSVTRSNLSLRDSDPPPARAQENGMPEE 120  
QY 121 PATTAGGPGKASRGFRFAGHSBAGGSGDRRRAGPEKPKSRREGSGGQESSRDKRPL 180  
DB 121 PATTAGGPGKASRGFRFAGHSBAGGSGDRRRAGPEKPKSRREGSGGQESSRDKRPL 180  
QY 181 SGPDVGTPOPGAGLASAKLAAGRPFNTYPRADTDHPSRAQOEPRHVAANGSAGGLAIP 240  
DB 181 SGPDVGTPOPGAGLASAKLAAGRPFNTYPRADTDHPSRAQOEPRHVAANGSAGGLAIP 240  
QY 241 QSSSSSRPTTRAGAPSPGVLGPHASEPOLAPACTPAAPVGPGRPSRORFORVS 300  
DB 241 QSSSSSRPTTRAGAPSPGVLGPHASEPOLAPACTPAAPVGPGRPSRORFORVS 300  
QY 301 HEQFRAALQLVDPGPRSYLNDNFIKIGSGTGVCIATVRSRSGKLVAVKMDLRKQRR 360

DB 301 HEQFRAALQLVDPGPRSYLNDNFIKIGSGTGVCIATVRSRSGKLVAVKMDLRKQRR 360  
QY 361 ELLFNEVIMRDYOHENNVEMNSYLVDGLVWMEFLLEGALTDIVTTRNMEQIAAV 420  
DB 361 ELLFNEVIMRDYOHENNVEMNSYLVDGLVWMEFLLEGALTDIVTTRNMEQIAAV 420  
QY 421 CLAVALQALSVLAQGVYIHRDIKSDSILLTHDGRVYKLSDFGCAQVSKVPRKSLVGTPT 480  
DB 421 CLAVALQALSVLAQGVYIHRDIKSDSILLTHDGRVYKLSDFGCAQVSKVPRKSLVGTPT 480  
QY 481 WMAPELISRLPYGPEVDIMSLGIMVLEWVDEPPYFNEPPLKAMKIRDLNLPRLKNLHK 540  
DB 481 WMAPELISRLPYGPEVDIMSLGIMVLEWVDEPPYFNEPPLKAMKIRDLNLPRLKNLHK 540  
QY 541 VSPSLKGFDRLLVRDPAQRATPAELIKHPFLAKAGPPASIVPLMRQNRTR 591  
DB 541 VSPSLKGFDRLLVRDPAQRATPAELIKHPFLAKAGPPASIVPLMRQNRTR 591  
RESULT 5  
US-09-949-016-6665  
; Sequence 6665, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE. METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: PatSeq for Windows Version 4.0  
; SEQ ID NO 6665  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6665  
Query Match 100.0%; Score 3090; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 3e-191;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFGKRRKRVISAPSNFEHVRHTGPDHOKFTGLPRWOSLIIESARRPKPLVDPACTT 60  
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QY 121 PATTAGGPGKASRGFRFAGHSBAGGSGDRRRAGPEKPKSRREGSGGQESSRDKRPL 180  
DB 121 PATTAGGPGKASRGFRFAGHSBAGGSGDRRRAGPEKPKSRREGSGGQESSRDKRPL 180  
QY 181 SGPDVGTPOPGAGLASAKLAAGRPFNTYPRADTDHPSRAQOEPRHVAANGSAGGLAIP 240  
DB 181 SGPDVGTPOPGAGLASAKLAAGRPFNTYPRADTDHPSRAQOEPRHVAANGSAGGLAIP 240  
QY 241 QSSSSSRPTTRAGAPSPGVLGPHASEPOLAPACTPAAPVGPGRPSRORFORVS 300  
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QY 301 HEQFRAALQLVDPGPRSYLNDNFIKIGSGTGVCIATVRSRSGKLVAVKMDLRKQRR 360  
DB 301 HEQFRAALQLVDPGPRSYLNDNFIKIGSGTGVCIATVRSRSGKLVAVKMDLRKQRR 360

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QY 361 ELLENVAVIMRDYOHENVVEMTNSYLVDGLVMVMEFLBEGALTDIVTHTRMNEEQIAAV 420
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Db 361 ELLENVAVIMRDYOHENVVEMTNSYLVDGLVMVMEFLBEGALTDIVTHTRMNEEQIAAV 420
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QY 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPT 480
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Db 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPT 480
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QY 481 WMAPELISRLPYGPEVDIVSLGIMVLEMDGEPYFNEBPPLKAMKIRDNLPRLKNLHK 540
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Db 481 WMAPELISRLPYGPEVDIVSLGIMVLEMDGEPYFNEBPPLKAMKIRDNLPRLKNLHK 540
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QY 541 VSPSLKGFDRLLVDRDPAQRATAAELIKHPFLAKAGPPASIVPLMRQNRTR 591
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Db 541 VSPSLKGFDRLLVDRDPAQRATAAELIKHPFLAKAGPPASIVPLMRQNRTR 591
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RESULT 6
US-09-949-016-7206
/ Sequence 7206, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ CURRENT APPLICATION NUMBER: US/09/949, 016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ NUMBER OF SEQ ID NOS: 2000-09-08
/ SOFTWARE: RastSeq for Windows Version 4.0
/ SEQ ID NO 7206
/ LENGTH: 620
/ TYPE: PRT
/ ORGANISM: Human
US-09-949-016-7206
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Query Match 100.0%; Score 3090; DB 4; Length 620;
Best Local Similarity 100.0%; Pred. No. 3,2e-191;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGRRKKRVEISAPSNFHHVHTGPDHOKTGLPRWQSLIESSARRPKLVDPACT 60
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Db 30 MFGRRKKRVEISAPSNFHHVHTGPDHOKTGLPRWQSLIESSARRPKLVDPACT 60
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QY 61 SIOPGAPKTTVRGSKAKDGLTLLDFEENMSVTRNSNLRDSPPPARARQENGMPEE 120
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Db 90 SIOPGAPKTTVRGSKAKDGLTLLDFEENMSVTRNSNLRDSPPPARARQENGMPEE 120
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QY 121 PATTAGGCGKAGSRFAGSEAGGSDRRRARRAPKPSRSGSGGPSSSRDRLPL 180
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Db 150 PATTAGGCGKAGSRFAGSEAGGSDRRRARRAPKPSRSGSGGPSSSRDRLPL 180
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QY 181 SGPDVGTPOGAGIAGKLAAGRPNFTYPRADTDHPSRGAQGEPHDVAFNGPSAGGLAIP 240
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Db 210 SGPDVGTPOGAGIAGKLAAGRPNFTYPRADTDHPSRGAQGEPHDVAFNGPSAGGLAIP 240
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QY 241 QSSSSSSRPPTARABSPGVLGPHASPOLAPACTPAAPAVGPGPSPPOREPORS 300
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Db 270 QSSSSSSRPPTARABSPGVLGPHASPOLAPACTPAAPAVGPGPSPPOREPORS 300
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QY 301 HEQFRAALQLVDPDPSYLDNFIKIGEGSTGVCIAATVRSSGKLVAVKMDLRKQORR 360
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Db 330 HEQFRAALQLVDPDPSYLDNFIKIGEGSTGVCIAATVRSSGKLVAVKMDLRKQORR 360
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QY 361 ELLENVAVIMRDYOHENVVEMTNSYLVDGLVMVMEFLBEGALTDIVTHTRMNEEQIAAV 420
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Db 390 ELLENVAVIMRDYOHENVVEMTNSYLVDGLVMVMEFLBEGALTDIVTHTRMNEEQIAAV 449
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QY 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPT 480
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Db 450 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPT 509
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QY 481 WMAPELISRLPYGPEVDIVSLGIMVLEMDGEPYFNEBPPLKAMKIRDNLPRLKNLHK 540
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Db 510 WMAPELISRLPYGPEVDIVSLGIMVLEMDGEPYFNEBPPLKAMKIRDNLPRLKNLHK 569
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QY 541 VSPSLKGFDRLLVDRDPAQRATAAELIKHPFLAKAGPPASIVPLMRQNRTR 591
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Db 570 VSPSLKGFDRLLVDRDPAQRATAAELIKHPFLAKAGPPASIVPLMRQNRTR 620
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RESULT 7
US-09-688-188B-30
/ Sequence 30, Application US/09688188B
/ Patent No. 6656716
/ GENERAL INFORMATION:
/ APPLICANT: PLOMAN, GREGORY
/ APPLICANT: MARTINEZ, RICARDO
/ APPLICANT: WHYTE, DAVID
/ TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
/ FILE REFERENCE: 038602/0328
/ CURRENT APPLICATION NUMBER: US/09/688, 188B
/ PRIOR FILING DATE: 2000-10-16
/ PRIOR APPLICATION NUMBER: 09/291,417
/ PRIOR FILING DATE: 1999-04-14
/ PRIOR APPLICATION NUMBER: 60/081,784
/ PRIOR FILING DATE: 1998-04-14
/ NUMBER OF SEQ ID NOS: 155
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 30
/ LENGTH: 398
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-688-188B-30
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Query Match 67.1%; Score 2073; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 5,8e-16;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 ASGAKLAARPNFTYPRADTDHPSRGAQGEPHDVAFNGPSAGGLAIPQSSSSSRPPTRA 253
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Db 1 ASGAKLAARPNFTYPRADTDHPSRGAQGEPHDVAFNGPSAGGLAIPQSSSSSRPPTRA 253
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QY 254 RGAPSPGVLGPHASPOLAPACTPAAPAVGPGPSPPOREPORSVHEQFRALQLVVD 313
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Db 61 RGAPSPGVLGPHASPOLAPACTPAAPAVGPGPSPPOREPORSVHEQFRALQLVVD 313
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QY 314 PGDPSYLDNFIKIGEGSTGVCIAATVRSSGKLVAVKMDLRKQORRELLFNEVAVIMRDY 120
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Db 121 PGDPSYLDNFIKIGEGSTGVCIAATVRSSGKLVAVKMDLRKQORRELLFNEVAVIMRDY 180
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QY 374 OHENVVEMTNSYLVDGLVMVMEFLBEGALTDIVTHTRMNEEQIAAVCLAVLQALSVLHA 433
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|
|
Db 181 OHENVVEMTNSYLVDGLVMVMEFLBEGALTDIVTHTRMNEEQIAAVCLAVLQALSVLHA 440
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|
QY 434 QGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPTYMAPELISRLPYG 493
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Db 241 QGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPTYMAPELISRLPYG 300
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|
QY 494 PEVDIVSLGIMVLEMDGEPYFNEBPPLKAMKIRDNLPRLKNLHKVSPSLKGFDRLL 553
|
|
|
Db 301 PEVDIVSLGIMVLEMDGEPYFNEBPPLKAMKIRDNLPRLKNLHKVSPSLKGFDRLL 360
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|
|
QY 554 VRDPAQRATAAELIKHPFLAKAGPPASIVPLMRQNRTR 591
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Db 361 VRDPAQRATAAELIKHPFLAKAGPPASIVPLMRQNRTR 398
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RESULT 8
US-09-291-417D-30
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; Sequence 30, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-30

Query Match      67.1%; Score 2073; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 5,8e-126;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 ASGAKLAAGRPFNTYPRADTDHPSRGAQGEPRHDVA PNGSAGGLAI PQSSSSSRPPTA 253
DB 1 ASGAKLAAGRPFNTYPRADTDHPSRGAQGEPRHDVA PNGSAGGLAI PQSSSSSRPPTA 60
QY 254 RGAPSGVGVPHASEPQLAPACTPAAPAVPGPPRS PORBPQVSHQFRAQLQVVD 313
DB 61 RGAPSGVGVPHASEPQLAPACTPAAPAVPGPPRS PORBPQVSHQFRAQLQVVD 120
QY 314 PGDPRLYDNFKIGSGTGVCIATVRSSGKLVAVKQDLRKQORRELLFNEVIMRDY 373
DB 121 PGDPRLYDNFKIGSGTGVCIATVRSSGKLVAVKQDLRKQORRELLFNEVIMRDY 180
QY 374 QHENVEMNSYVQGEIWMVMEFLGGLTDIVTTRNMEBOIAVCLAVLQALSVLVA 433
DB 181 QHENVEMNSYVQGEIWMVMEFLGGLTDIVTTRNMEBOIAVCLAVLQALSVLVA 240
QY 434 QGVYHDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRSKLVGTPLYMAAPELISRLPYG 493
DB 241 QGVYHDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRSKLVGTPLYMAAPELISRLPYG 300
QY 494 PEVDIWSLGIWIEWDGEPYFNEBPPLKAMKMI RNDLPPRLKNLHKVSPSLKGFIDRLI 553
DB 301 PEVDIWSLGIWIEWDGEPYFNEBPPLKAMKMI RNDLPPRLKNLHKVSPSLKGFIDRLI 360
QY 554 VRDPAQRATRAELIKHPFLAKAGPPASIVPLMRQNR 591
DB 361 VRDPAQRATRAELIKHPFLAKAGPPASIVPLMRQNR 398

RESULT 9
US-09-688-188B-29
; Sequence 29, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 681
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-188B-29

Query Match      47.7%; Score 1473.5; DB 4; Length 681;
Best Local Similarity 48.1%; Pred. No. 4.2e-87;
Matches 331; Conservative 69; Mismatches 169; Indels 119; Gaps 12;

QY 4 KKKRVEISAPSNFERRVHTGPDQHEQKGTGLPRQMSLIIESARPKLYVPACTTSIQ 63
DB 5 KKKRVEISAPSNFERRVHTGPDQHEQKGTGLPRQMSLIIESARPKLYVPACTTSIQ 63
QY 64 PAPKTIYVSGSGADGALTLLDDEFENMSYRSNSLRDSDPPPARAR----- 112
DB 64 LQPMKTIYVSGSAMPDVGTISGLNDIQKLSVSSNITLRGRSTRRRAOSLGLGDHHA 123
QY 113 -----QENGM-----PEBPATTARGPGKAGSG-- 136
DB 124 TDPDNYLQSGPQERTDPHGLVYLSGNGTPAGHKQMPWPQSPRYL PNGLAAKAQSIGPA 183
QY 137 RRAHSEAG--GSGDRRRAGPEKRPKSSRGSGGPGQSSSKDKPPLS-----GP 183
DB 184 EFGQASQRCLOAGACIQSSPPGASPPGTNRHGMRAAKHGSSEARPOSLVGSATGRPG 243
QY 184 DVGTPQAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPRHDVA PNGSAGGLAI PQSS 243
DB 244 E-GSPSPKTRBSLKRRLFRSM-FLSTATAPSSSKPEPPQSKFN----- 288
QY 244 SSSSRP-----TRARGAPSP---GVLGPHASEPQLAPACTPAAPAVPGPPRS 291
DB 289 -SSFRPQKDNPSLVAKAQSILPSDQPVGTSPPLTTSIDTSSQKSLRTAPATQGLPGRSS 347
QY 292 PQREPOR-----VSHQFRAQLQVVDPGDPRLY 321
DB 348 PAPSPTTQAQISTSNLYLPQDPVYAKGALAGEDTGVTHQFKAIRVVYVQGPRLI 407
QY 322 DNPRIKGGSTGIVCIATVRSSGKLVAVKQDLRKQORRELLFNEVIMRDYQHENVEM 381
DB 408 DSVYKIGBSTGIVCIATVRSSGKLVAVKQDLRKQORRELLFNEVIMRDYQHENVEM 467
QY 382 YNSYVQGEIWMVMEFLGGLTDIVTTRNMEBOIAVCLAVLQALSVLHAQVYHDI 441
DB 468 YNSYVQGEIWMVMEFLGGLTDIVTTRNMEBOIAVCLAVLQALSVLHAQVYHDI 527
QY 442 KSDSILLTHDGRVKLSDFGCAQVSKEVPRRSKLVGTPLYMAAPELISRLPYG 501
DB 528 KSDSILLTHDGRVKLSDFGCAQVSKEVPRRSKLVGTPLYMAAPELISRLPYG 587
QY 502 GIMVIEWDGEPYFNEBPPLKAMKMI RNDLPPRLKNLHKVSPSLKGFIDRLI VRDPAQRA 561
DB 588 GIMVIEWDGEPYFNEBPPLKAMKMI RNDLPPRLKNLHKVSPSLKGFIDRLI VRDPAQRA 647
QY 562 TAAELIKHPFLAKAGPPASIVPLMRQNR 589
DB 648 TAAELIKHPFLAKAGPPASIVPLMRQNR 675

RESULT 10
US-09-291-417D-29
; Sequence 29, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
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```

; SEQ ID NO 29
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-29

```

```

Query Match      47.7%; Score 1473.5; DB 4; Length 681;
Best Local Similarity 48.1%; Pred. No. 4.2e-87;
Matches 331; Conservative 69; Mismatches 169; Indels 119; Gaps 12;

```

```

QY 4 KRKRVESAPSNFEHRTVTGPDQHEQKFTGLPRQMSLIESARPPKLVDPACTISIQ 63
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 5 KKKRREISAPQNFQHRVHTSPDKGKFGVGLPPQWNTL-DTLRPPKVVDPSSRITRVQ 63
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 64 PGAKTIVRGSKAKOGALTLTLLDEFENMSVTRNSLRDSDPPPARAR----- 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 64 LQPMKTVRGSKAMPVDYIISGLNDYOKLSVISNTLRGSPTRRRRAQSLGLGDEHMA 123
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 113 -----OENGM-----PEBPATTARGGPGKAGSRG-- 136
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 124 TDDPMYLOSPOSERTPDHGLYLSGNGGTPAGHKQMPWEPQSPRVLPNGIAAKAQSIGPA 183
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 137 RPAHSEAG--GSGDRRRAAGPEKRPKSSREGSGPQESSRDKRPIS-----GP 183
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 184 EFOGASORCLQGLGACLOSPPGASPTGTNRHGKMAKAGSEARPOSLVGSATGRPG 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 184 DVGTPQAPGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVAENGPSAGGLAIPQSS 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 244 E-GSPSPKTRRESSLKRLFRSM-FLSTAAATAPRSSSKRPQSKPN----- 288
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 244 SSSSRPP-----TRAGABSP--GYLAGPHASEPQLAPACTPAAPAVPGPPGRS 291
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 289 -SSFRPPQKDNPPSLVAKAQLPSDQPVGTFTSPLTTSSTSSPKSLRTAPATGQLPGRSS 347
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 292 PQREPQR-----VSHQOPRAALQLVVPDPPRSYL 321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 348 PAGESPRTHMAQISTNSNLYLPDDPTVAKGALAGEDTVGTHQFALRMVVDDQDPRLLL 407
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 322 DNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQRRLLFNEVYIMDYOHENYEM 381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 408 DSYKIVIGEGSTGIVCLAREKISGRQVAVKMDLRKQRRLLFNEVYIMDYOHFNVENM 467
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 382 YNSYIVGDELMVWMEFLGGLTDTIVHTNNEBOIAVCLAVYQALSVLAQGVIRDI 441
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 468 YKSYIVGDELMVWMEFLGGLTDTIVSQVRLNEBOIATVCEAVYQALAYLAQGVIRDI 527
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 442 KSDSILLTHDGRVKLSDFGCAQVSKVEYPRRKSIVGTIPYMAPELISRLPYGPEVDIWSL 501
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 528 KSDSILLTHDGRVKLSDFGCAQISKQVPRKKSIVGTIPYMAPEVISRSLYATEVDIWSL 587
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 502 GIMVIEVMDGEPYPNEPPLKAMKIRDNLPRLKNLHKVPSLSKGLFDRLVNDPAPORA 561
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 588 GIMVIEVMDGEPYPNSDPSVQAMKRLRDSPPKLNKSHKVSPLVRLFLERMLVNDPORA 647
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 562 TAAELIKHPFLAKAGPPASIVPLMRONR 589
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 648 TAAELIDHPFLQTLGPECLVPLQLYR 675
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 11
US-09-949-016-10445
; Sequence 10445, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10445
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10445

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Query Match      47.7%; Score 1473.5; DB 4; Length 694;
Best Local Similarity 48.1%; Pred. No. 4.3e-87;
Matches 331; Conservative 69; Mismatches 169; Indels 119; Gaps 12;

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QY 4 KRKRVESAPSNFEHRTVTGPDQHEQKFTGLPRQMSLIESARPPKLVDPACTISIQ 63
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 18 KKKRREISAPQNFQHRVHTSPDKGKFGVGLPPQWNTL-DTLRPPKVVDPSSRITRVQ 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 64 PGAKTIVRGSKAKOGALTLTLLDEFENMSVTRNSLRDSDPPPARAR----- 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 77 LQPMKTVRGSKAMPVDYIISGLNDYOKLSVISNTLRGSPTRRRRAQSLGLGDEHMA 136
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 113 -----OENGM-----PEBPATTARGGPGKAGSRG-- 136
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 137 TDDPMYLOSPOSERTPDHGLYLSGNGGTPAGHKQMPWEPQSPRVLPNGIAAKAQSIGPA 196
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 137 RPAHSEAG--GSGDRRRAAGPEKRPKSSREGSGPQESSRDKRPIS-----GP 183
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 197 EFOGASORCLQGLGACLOSPPGASPTGTNRHGKMAKAGSEARPOSLVGSATGRPG 256
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 184 DVGTPQAPGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVAENGPSAGGLAIPQSS 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 257 E-GSPSPKTRRESSLKRLFRSM-FLSTAAATAPRSSSKRPQSKPN----- 301
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 244 SSSSRPP-----TRAGABSP--GYLAGPHASEPQLAPACTPAAPAVPGPPGRS 291
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 302 -SSFRPPQKDNPPSLVAKAQLPSDQPVGTFTSPLTTSSTSSPKSLRTAPATGQLPGRSS 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 292 PQREPQR-----VSHQOPRAALQLVVPDPPRSYL 321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 361 PAGESPRTHMAQISTNSNLYLPDDPTVAKGALAGEDTVGTHQFALRMVVDDQDPRLLL 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 322 DNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQRRLLFNEVYIMDYOHENYEM 381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 421 DSYKIVIGEGSTGIVCLAREKISGRQVAVKMDLRKQRRLLFNEVYIMDYOHFNVENM 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 382 YNSYIVGDELMVWMEFLGGLTDTIVHTNNEBOIAVCLAVYQALSVLAQGVIRDI 441
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 481 YKSYIVGDELMVWMEFLGGLTDTIVSQVRLNEBOIATVCEAVYQALAYLAQGVIRDI 540
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 442 KSDSILLTHDGRVKLSDFGCAQVSKVEYPRRKSIVGTIPYMAPELISRLPYGPEVDIWSL 501
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 541 KSDSILLTHDGRVKLSDFGCAQISKQVPRKKSIVGTIPYMAPEVISRSLYATEVDIWSL 600
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 502 GIMVIEVMDGEPYPNEPPLKAMKIRDNLPRLKNLHKVPSLSKGLFDRLVNDPAPORA 561
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 601 GIMVIEVMDGEPYPNSDPSVQAMKRLRDSPPKLNKSHKVSPLVRLFLERMLVNDPORA 660
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 562 TAAELIKHPFLAKAGPPASIVPLMRONR 589
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 661 TAAELIDHPFLQTLGPECLVPLQLYR 688
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 12
US-09-765-815-2
; Sequence 2, Application US/09765815
; Patent No. 6673586
; GENERAL INFORMATION:
; APPLICANT: Balk, Steven
; TITLE OF INVENTION: No. 6673586e1 Steroid Hormone Receptor
; TITLE OF INVENTION: Interacting Protein Kinase
; FILE REFERENCE: 01948/068002

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; CURRENT APPLICATION NUMBER: US/09/765, 815
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 66/176, 859
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-765-815-2

Query Match          47.6%; Score 1470.5; DB 4; Length 681;
Best Local Similarity 48.0%; Pred. No. 6,5e-87;
Matches 330; Conservative 70; Mismatches 169; Indels 119; Gaps 12;

QY 4 KKKKVEISAPSNFEHRTGPDQHEOKFTGLPRQWOSLIEESARRPKLVDPACTISIQ 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 5 KKKKREIISAPQVFOHRTVHTSPDKGKFKVGLPPQMNIL-DTLRRPKPVDPDSRITRVQ 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 PGAPKTIYSGSKAKXGALTLILLDEFENNVTSNSLRDPPPPARAR----- 112
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 64 LQPKTIYVSGSNAMPVGVYISGLINDIQKLSVSSNTLRGSRPSRRRAQSLGLGDEHMA 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 113 -----GNGM-----PEEPATTARGGPGKAGSRG-- 136
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 124 TDPMYLGSPQSRTPRHGILYSCNGTTPAGHKQMPPEQSRVLNGLAQAQSLGPA 183
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 137 RFAGHSAG--GSGDRRRAGPEKRRKSSREGSGQESRDRLPLS-----GP 183
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 184 EFGAGQRCLOLQACLOSPPGASPTGTNRHGMKAKAKHSEARPOSCLVGSATGRPGG 243
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 184 DVCTPQAGLASAKLAAGRPNTYPRADTDHPSRGAQSEPHVAENPGSAGGLAIPQSS 243
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 244 E-GSPSPKTRSSLRKRLFFSM-FLSTAAATAPSSSKPPGPPQSKPN----- 288
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 244 SSSSRPP-----TRAGARSP--GVLGPHASBPQALAPACTPPAFAVPPGPPRS 291
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 289 -SSFRPPQKDNPPSLVAKAKQSLPSDQVGTFFSLTSDTSFQKSLRTAPATQQLFRSS 347
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 292 POREPQ-----VSHQPRALQLVVDPPDRSYL 321
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 348 PAPSPTWHAQISTNLYLPQDPTVAKGALAGEDTVGVTHQKALRMVVDGDDRLLL 407
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 322 DNTIKIGESGTGVCIAATVRSAGLVAAVKMDLRKQORRLNEVYIMRDYHENVEM 381
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 408 DSIVKIGESTGTVCIAAREKHSRGVAAVKMDLRKQORRLNEVYIMRDYHENVEM 467
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 382 YNSYLVDGLVMVMEFLGEGALTDIVTHTRMNEEOIAAVCLAVLQALSVLHAQGVHRI 441
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 468 YKTYLVGDELVMVMEFLQGGALTDIVSQVRLNEEOIATVCEAVLQALVLAQGVHRI 527
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 442 KSDSILLTHDGRVXLSDFGCAQVSKVPRKSLVGTPTWMAPELISRLPYGPEVDIWSI 501
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 528 KSDSILLTLTDGRVXLSDFGCAQISKDVPRKSLVGTPTWMAPEVLSRLIATEVDIWSI 587
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 502 GIMVIMVNDGEPPEYFNEPPLKAMKMTIDNLPPLKLNHKSPLSKGFLDRLVDPQAQRA 561
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 588 GIMVIMVNDGEPPEYFSDSPVQAKMRKLDSPPLKLNHKSPLSKGFLDRLVDPQERA 647
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 562 TAAELKHPFLAKAGPPASIVPLMRQNR 589
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 648 TAOELDHPFLQDTGLPECLVPLIQLYR 675
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-09-082-737-3
; Sequence 3, Application US/09082737
; Patent No. 6013500
; GENERAL INFORMATION:
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK4; A No. 6013500el Gene Encoding A Serine/
; TITLE OF INVENTION: Threonine Kinase
```

```
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11230
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,737
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/55311
; TELECOMMUNICATION INFORMATION:
; TELEFAX: (212) 391-0525
; TELEPHONE: (212) 278-0400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-082-737-3

Query Match          41.3%; Score 1277; DB 3; Length 250;
Best Local Similarity 99.6%; Pred. No. 6e-75;
Matches 249; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 324 FIKIGSGTGVCIATVRSAGLVAAVKMDLRKQORRLNEVYIMRDYHENVEM 383
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DB 1 FIKIGSGTGVCIATVRSAGLVAAVKMDLRKQORRLNEVYIMRDYHENVEM 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 384 SYLVGDELVMVMEFLGEGALTDIVTHTRMNEEOIAAVCLAVLQALSVLHAQGVHRI 443
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 SYLVGDELVMVMEFLGEGALTDIVTHTRMNEEOIAAVCLAVLQALSVLHAQGVHRI 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 444 DSILLTHDGRVXLSDFGCAQVSKVPRKSLVGTPTWMAPELISRLPYGPEVDIWSI 503
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 DSILLTHDGRVXLSDFGCAQVSKVPRKSLVGTPTWMAPELISRLPYGPEVDIWSI 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 504 WTEWVDGEPPEYFNEPPLKAMKMTIDNLPPLKLNHKSPLSKGFLDRLVDPQAQRA 563
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 WTEWVDGEPPEYFNEPPLKAMKMTIDNLPPLKLNHKSPLSKGFLDRLVDPQAQRA 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 564 AELKHPFLA 573
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 AELKHPFLA 250
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RESULT 14
US-09-718-032-3
; Sequence 3, Application US/09718032
; Patent No. 6667168
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK4; A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
; FILE REFERENCE: 575/55311-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/718,032
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: PCT/US99/11341
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 09/082,737
; PRIOR FILING DATE: 1998-05-21
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; ; NUMBER OF SEQ ID NOS: 17
; ; SOFTWARE: PatentIn version 3.1
; ; SEQ ID NO 3
; ; LENGTH: 250
; ; TYPE: PRF
; ; ORGANISM: human
US-09-718-032-3

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Query Match	41.3%	Score 1277	DB 4	Length 250
Best Local Similarity	99.6%	Pred. No. 6e-75		
Matches 249; Conservative	0	Mismatches 1	Indels 0	Gaps 0

Qy	32	FIKIGESGTCIVCIATVRSSGKLVAVKMDLKKOORRELLPNEVAVIMRDVQHEHNVEMYN	383
Db	1	FIKIGESGTCIVCIATVRSSGKLVAVKMDLKKOORRELLPNEVAVIMRDVQHEHNVEMYN	60
Qy	384	SYLVGBELVWVMEFLFGALTDIVTHTRNNEEQIAVCAVLQALSVLHAGVTHRDIKS	443
Db	61	SYLVGBELVWVMEFLFGALTDIVTHTRNNEEQIAVCAVLQALSVLHAGVTHRDIKS	120
Qy	444	DSILLTHDGVKLSDFGFCQAVSKVYPRKKSIVGTPYMAPELISRLPYGPEVDIWSLGI	503
Db	121	DSILLTHDGVKLSDFGFCQAVSKVYPRKKSIVGTPYMAPELISRLPYGPEVDIWSLGI	180
Qy	504	MVLEMVDGEPYNEPPLKAMKIMIRDNLPRLKNIHKVSPSLKGFLLRDLVRODPAQRATA	563
Db	181	MVLEMVDGEPYNEPPLKAMKIMIRKNLPRLKNIHKVSPSLKGFLLRDLVRODPAQRATA	240
Qy	564	AEILKTPFLA 573	
Db	241	AEILKTPFLA 250	

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RESULT 15
US-08-935-760-2
: Sequence 2, Application US/08935760A
: Patent No. 5952217
: GENERAL INFORMATION:
: APPLICANT: Gorman, Jessica A.
: APPLICANT: Manly, Susan
: TITLE OF INVENTION: Recombinant Yeast Cell and Assay Using Same
: FILE REFERENCE: ON0156sequence
: CURRENT APPLICATION NUMBER: US/08/935,760A
: CURRENT FILING DATE: 1997-09-23
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 544
: TYPE: PRT
: ORGANISM: Rattus exulans
US-08-935-760-2

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Query Match	29.5%	Score 912	DB 2	Length 544
Best Local Similarity	35.7%	Pred. No. 4.5e-51		
Matches 210; Conservative	87	Mismatches 166	Indels 126	Gaps 8

Qy	4	KKKKKVLSANPSNFEHRVNTGPDQHEQKQTGLPRQMSLIE-----ESARRKPLVDP	56
Db	63	KKKRRPRLSPSPDSEHTIHVGPDVATGEPTGLPEQMAILLTQNTYKLEQKKNQAVLD-	121
Qy	57	ACITTSIOPGAPKTIIVGSSKAGDQGLTLLDLDFENMSTYTRNSLRDRSPPPARAQENG	116
Db	122	-----VLKRYDSKETLVNNQKXMSFT-----	141
Qy	117	MPEEPATTANGGPKGKSGRFRAGHSSEAGSGSGDRRRAQPEKRPKSPHESGGQFQSSRD	176
Db	142	-----SGDKSAHGVIYAHQ-----SNTTAASEPPLAPVSEEDDEEEDEEDD	184
Qy	177	KRPLSGPDVGTPOPAIGLASGAKLLAGRPENTYPRADTQHPKSGAQGSEHDVAVPSGAGG	236
Db	185	NEP---PPIAIPPEPHTKS-----IYTRKVESIASPA-----APPKKATPP	223
Qy	237	LAIPQSSSSSSRRPTARGAPSPGVLGPHASEPOLAPACTPAAPAVGPPGPRSPQREP	296

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Db      224  SAEANANSTIYKRTIDR-----QRKK 243

Qy      297  QRVSHQFRALQIYVDPGDPSPSYLDNFIKIGEGSTGIVCIATVRSRGKLVAKKMDLRK 356
      244  SKMTDEEILFKRSIYVSGDPKKKTYTRFEKIGQGSATGVYALDIANGOEVAIKOMNLQO 303

Qy      357  QQRRELLFNEVYIMRQYCHENVEWYMSYVGDLMVYMEFLBEGALTDIYTHRRMEEQ 416
      304  QPKKELINIIIVRENNKNPNIVNYSLDVGBELVMMEFLAGSGLDVIYETCMBEQ 363

Qy      417  IAAVCLAVIALSVLHAQGVIRHDIKSDSIYLLTHEDGRVYKLSDFGCAQVSKENYPRRSYLV 476
      364  IAAVCBECLQALDFLHNSQVYHRDIKMDNIILGMDGSVKYLDPFQCAQITPEQSKRSTW 423

Qy      477  GTPYMAPELISLRYGPEVNDIWSIGIYVIEKWDGEPYFNEPPLKAMKMIKRNLPRLK 536
      424  GTPYMAPEVYVTRKAYGKVDIWSIGIYVIEKWDGEPYFNEPPLKALYIATNGTPELO 483

Qy      537  NUKHVSLSLKGFLDRLLVDPDQAKRTAAEILKHPRLAAGRPASIVPELM 585
      484  NPEKLSVAFDFPLNRCLENDVDRKSAEELQHPRLKIAKLAKLUSLTPLIT 532

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Search completed: March 15, 2005, 11:32:29  
Job time : 55.1471 secs